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FILE COVERS 1907 - 13 Feb 2003 VOL 138 ISS TELE LAST UPDATED: 12 Feb 2003 (20030212/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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LT AMSWER 1 OF 1 HOAPLUS COPYRIGHT 2003 A08 ACCESSION NUMBER: 2000:535163 HOAPLUS

DOCUMENT NUMBER: 133:145915

TITLE: Transcription factor E2F DNA-binding domain inhibitor

peptides and uses thereof

INVENTOR(S): Muller, Rolf; Kontermann, Roland Ernst; Montigiani,

Silvia

PATENT ASSIGNEE(S): Prolifix Limited, UK SOURCE: PCT Int. Appl., 42 pp.

CODEN: FIRMEL

DOCUMENT TYFE: Fatent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

SE, JL, TJ, TE, TE, IT, TJ, JE, IV, IV, IV, IV, IV, JE, IV, JE, AZ, EY, KJ, KL, KL, ST, TJ, TK RW: GH, GM, KE, LS, MW, SD, SL, GD, TZ, UG, EW, AT, PE, CH, CY, LE, DK, ES, FI, FR, GB, GR, IE, II, LU, MD, ML, ET, GE, EF, EJ, GF, CA 2359143 AA 2 1813 AA 2011-2359143 A 171126 EF 1144437 A1 20 11017 EF 201-201225 20 12 126 E: AT, BE, CE, DE, DE, ES, FR, SF, 48, IT, L1, LU, NU, SE, MU, FT, 1E, SI, LT, LT, F1, B0 us 2003013109 | A1 | 1.7730110 77 0 1-912414 2 0.7726 GB 1999-1710 A 19990126 PRIORITY APPLN. INFO.: WO 2000-GB227 W 20000126 OTHER SOURCE(S): MARPAT 133:145915The present invention provides sequences of peptides which bind to the DNA binding domain of transcription factor E2F, and inhibit cell cycle progression. Peptides include FWLRFT, WVRWHF, WHFIFW, IWLSGLSRGVWVSFF, and GSRILTFRSGSWYAS and derivs. based upon these sequences. Compns. and the use or the peptides in inhibiting sell sysle progression, such as in uncontrolled cell proliferation, are also provided. 286839-16-5P RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRF (Properties); SPM (Synthetic preparation); BIOL (Biological study); OCCU (Goourrence); PREP (Preparation); TSES (Tses opeptide sequence; transcription factor E2F DNA-bin ling schain inhibitor peptides and uses thereof, 286839-22-3 286839-23-4 RI: FRF (Properties) unclaimed sequence; transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof) REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT => select hit rn 17 1 El THROUGH ES ASSIGNED => fil red FILE 'REGISTRY' ENTERED AT 13:50:51 ON 13 FEB 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Chemical Society (ACS) Property values tagged with IC are from the CDT VIIIITL as a 1700 provided by into hom. STRUCTURE FILE UPDATES: 12 FEB 2005 HIGHBUT BN 489386-00-1 DICTIONARY FILE UPDATES: 12 FEB 2003 HIGHEST RN 489395-53-1 TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002 Please note that search-term pricing does apply when condusting SmartSELECT sear thes. Crossover limits have been increased. See HELP CROSSOVER for details. Emperimental and calculated property data are now available. See HELP FROFERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:

http://www.cas.org/ONLINE/STN/STNOTES stnotes00.pdf

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LII ANSWER 1 OF 26 HCAPLUS COPYRIGHT 2003 ACS
                         2002:850304 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         137:347570
                          Cloning and cDNA and deduced amino acid sequences of
TITLE:
                          69 human proteins and their diagnostic and therapeutic
                          uses
INVENTOR (S):
                         Ruben, Steven M.; Barash, Steven J.; Bosen, Traid A.;
                         Birse, Charles A.
PATENT ASSIGNEE(S):
                         Human Genome Sciences, Inc., USA
                          U.S. Pat. Appl. Publ., 194 pp., Cont.-in-part of Appl.
SOURCE:
                          No. POT/US01/01346.
                         CODEN: USMKCO
DOCUMENT TYPE:
                         Patent
                         English
LANGUAGE:
FAMILY ACC. NUM. COUNT: 90
PATENT INFORMATION:
     PATENT NO. KIND DATE
                                            APPLICATION NO. DATE
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     US 2002165137 A1 20021107
WO 2001055449 A1 20010802
                                            US 2001-860670
                                                              20010521
                                          WO 2001-US1346
                                                              20010117
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US 2000-241809P P 20001020
US 2000-244617P P 20001101
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TS 3000-251356F P 20001208
US 2000-251868P P 20001208
US 2000-251869P P 20001208
US 2001-764863 B1 20010117
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The present invention relates to 69 novel human proteins and isolated AB nucleic acids contg. the coding regions of the genes encoding such proteins. Tissue distribution, sequence nomologies, and preferred epitope sites are provided for the proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human proteins. High-throughput screening assays are also provided for various putative activities of the proteins.

474183-38-5P, Protein (human clone HFIED13) FL: BPN (Biosynthetic preparation ; BSU (Biological study, unclassified); DGN (Dlagnostld use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; cloning and cDNA and deduced amino acid sequences of 69 numan proteins and their diagnostic and therapeutic uses)

L11 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2003 ACS ADDESSION NUMBER: 2002:723249 HCAPLUS

137:227411 DOCUMENT NUMBER:

Whole-genome comparison of Mycobacterium tuberculosis TITLE:

clinical and laboratory strains

AUTHOR(S): Fleischmann, R. D.; Alland, D.; Eisen, J. A.;

> Carpenter, L.; White, O.; Peterson, C.; DeBoy, R.; Dodson, E.; Gwinn, M.; Haft, D.; Hickey, E.; Kolonay, J. F.; Nelson, W. C.; Umayam, L. A.; Ermolaeva, M.; Salzherg, S. L.; Delcher, A.; Utterback, T.; Weidman, J.; Fhouri, H.; Gill, J.; Mikula, A.; Bishai, W.;

Jacobs, W. R., Jr.; Venter, J. C.; Fraser, C. M. The Institute for Genomic Research, Rockville, MD,

20880, USA

SOURCE:

American Society for Microbiology PUBLISHER:

Journal DOCUMENT TYPE: English LANGUAGE:

CORPORATE SOURCE:

Virulence and immunity are poorly understood in Mycobacterium tuberculosis. The complete denome of the M. tuberculosis clin. strain CDC1551 was sequences and a whole-genome comparison with the lab. strain HiTRy performed in order to identify polynumbhic sequences with potential relevance to disease pathogenesis, immunity, and evolution. large-sequence and single-nuclectide polymorphisms were found in numerous genes. Polymorphic loci included a phospholipase C, a membrane lipoprotein, members of an adenylate cyclase gene family, and members of the FE'PPE gene family, some of which have been implicated in virulence or the host immune response. Several gene families, including the PE/PFE gene family, also had significantly higher synonymous and nonsynonymous

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substitution frequencies communed to the denome as a whole. A large sample of M. tuberculosis ofin. isolates was tested for a subset of the large-sequence and single-nuclectide polymorphisms and widespread genetic variability was found at many of these loci. Phylogenetic and epidemiol. anal, was parmied out to investigate the evolutionary relationships among isolates and the origins of specific polymorphic loci. A no. of these y lymorphisms appear to have obsurred multiple times as independent events, suggesting that these ununges may be under selective pressure. Tugether, these results demonstrate that polymorphisms among M_{\star} tuberculosis strains are more extensive than initially antibipated, and genetic variation may have an important role in disease pathogenesis and immunity. The sequence of the clin. strain CDC1551 of M. tuberculosis was deposited in GenBank/EMBL/DDBJ under accession no. AE000516, and the sequence of the genome of the M. tuberrultsis lab. strain H87kv was recently sequenced and deposited as NO 97, 962.

457684-48-9

RL: BSU (Bicligibal study, undiassines; PF) (Frigertie); Pf)) (Biological study)

\amino acid sequence; whole-genome comparison of Mycobacterium tuberculosis clin. and lab. strains'

REFERENCE COUNT:

42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 26 HOAPLUS COPYRIGHT 2003 ACS 2002:545718 HOAPLUS 137:74287

DOCUMENT NUMBER:

TITLE:

AUTHOR(S):

lateral gene transfer between bacteria and Archaea Deppenmeier, Uwe; Johann, Andre; Hartsch, Thomas; Merkl, Rainer; Schmitz, Ruth A.; Martinez-Arias, Rosa; Henne, Anke; Wiezer, Arnim; Baumer, Sebastian; Jacobi, Carsten; Bruggemann, Holger; Lienard, Tanja; Christmann, Andreas; Pomeke, Mechthild; Steckel, Silke; Bhattacharyya, Anamitra; Lykidis, Athanasios; Overbeek, Ross; Klenk, Hans-Feter; Gunsalus, Robert F.; Fritz, Hans-Joachim; Gottschalk, Gerhard

Gottingen Genomics Laboratory. Department of General

Microbiology. Institute of Microbiology and Genetics,

The genome of Methanosarcina mazei: evidence for

CORPORATE SOURCE:

SOURCE:

PUBLISHER:

Georg-August-University, Goethingen, D-37 NOT, Germany Cournal of Molecular Microbiology and Biotechnology (2002), 4(4), 453-461

0.DEM: JAMEFF; IS.M: 1464-1801 Horizon Scientific Fress

DOCUMENT TYPE: Journal English LANGUAGE:

The Archaeon Methanosardina mazei and related species are of great edol. importance as they are the only organisms fermenting acetate, methylamines and methanol to methane, carbon dioxide and ammonia (in case of methylamines). Since acetate is the precursor of 60° of the methane produced on earth these organisms contribute significantly to the prodn. of this greenhouse gas, e.g. in rice gaddies. The 4,096,340 base pairs circular chromosome of M. manel is more than twice as large as the genomes of the methanogenic Archaea currently completely sequenced. There were 3371 open reading frames (ORFs) identified. Based on currently available sequence data 376 of these ORFs are Methanosardina-specific and 1043 ORFs find their closest homolog in the batterial domain. About 544 of these ORFs reach significant similarity values only in the bacterial icrain. They include 34 of the 1 cotransposes of an improve continuous in singular products, particular and equivariate thoughts and the control of the pair, environmental sending, general pulation, and etheron or gonder. Otherwing examples are the coordinative of the harderful Großlich Ed maper in system and the presence of tetrahydr islate-ampendent encymes. These lindings might indicate that lateral gene transfer has played an important

evolutionary role in forming the physical of this metabolically versatile methanogen. The genome sequence is deposited in JenBank under Arression No. AEGJ8384.

440301-84-8

RL: BSU Biological study, unclassified; FFF Fregerties; BIOL Biological study;

damino adid sequence; complete genome sequence of Methanisar condition
and evidence for lateral gene transfer between bacteria and Archaea

REFERENCE COUNT:

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REFERENCE COUNT:

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L11 ANSWER 4 OF 26 HOAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:348600 HOAPLUS

DOCUMENT NUMBER: 137:28983

TITLE: Euman genome derived single exon nucleic acid probes

useful for gene empression analysis

INVENTOR(S): Penn, Sharron Gaynor; Rank, David Russell; Chen,

Wenshen: Hanzel, David Kagen

PATENT ASSIGNEE (S): USA

SOURCE: U.S. Fat. Appl. Fubl., 97 pp., Cont.-in-part of U.S.

Ser. No. 774,203.

CODEN: USXXCO

DOCUMENT TYPE: Patent LANGUAGE: English FAMILY ACC. NUM. COUNT: 84

PATENT NO.	MINI DATE	Arini Walling.	
US 2002048763 GB 2360284 GB 2360284	A1 20020425 A1 20010919 B2 20020227	US 2001-864761 GB 2000-24263	20010523 20001004
GB 2361238 GB 2361238	A1 20(11017 B2 20(20306	GB 2001-15281	20001004
US 2002081590 We 2001081270	A1 20(20627 A2 20(10809	US 2001-774203 WO 2001-US661	20010129 20010130
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UTY APPLN. INFO.: US 2000-180312P P 20000204
PRIORITY AFPLN. INFO.:
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                                     TS 2000-60840A AD 00100080
                                     TS 2000-632366 AZ 20000643
                                     US 2000-234657P P 200009%1
                                     US 2000-236359P P 20000927
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                                     US 2001-774203 A2 20010129

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      A2 20010130

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      A2 20010130

                                     WO 2001-US663 A2 20010130
                                     Wo 2001-US665 A2 20010180

    WG 2001-US666
    A2 0001018

    WG 2001-US667
    A2 20010130

                                     MO 2001-US668 A2 20010180
                                     WO 2001-US669 A2 20010130
                                     WO 2001-US670 A2 20010130
                                     TS 2001-166860P P 20010208
    Methods and app. for predicting, contirming and displaying functional
AB
    regions from genomic sequence data are used to identify 16,834 unique
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human genome-derived single exon probes useful for gene expression anal., particularly gene expression anal. by microarray. Also presented are genome-derived single exon microarrays that include such probes, peptides encoded by the exons, and antibodies thereto. The human genome-derived single-exch probes are known to be expressed in one or more human tissues or dell types, particularly human brain, neart, liver, fetal liver, placenta, lung, bone marrow, BT474 and other human mammary epithelial cells, HeLa and other human cervical epithelial cells, and HBL 100 and other human mammary epithelial cells. The invention provides a method of financing, selling and/or licensing genome-derived single-exon microarrays to customer desiring to measure gene expression, comprising: making available for computerized query or subscription service a database having a record corresponding to each genome-derived single exch microarray available for sale and or litense. [This abstr. record is one of ten records for this document newssitated by the lines no. I index entries required to fully index the a common magazineth or year constraints. \.

II 437115-91-8

RL: BSU (Biological study, unclassified); FRF (Froperties); BIOL (Biological study)

(amino abid sequence; human genome derived single exon nucleic acid probes useful for sene expression anal.)

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LII ANSWER 5 OF 06 HOAFLUS COFYRIGHT 2003 ACS
ACTRIVIOU NUMBER: 2 01:08385 HOAFLUO
DESUMENT NUMBER: 100:08385 HOAFLUO
TITLE: 2 complete genome sequence of Methanosardina abetivorans
C2A reveals extensive metabolic and physiological
diversity
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ETTHER :

Callerian, Camboo E.; Mostalar, Char, Bow, Aller, Endriczi, Marthew B.; Martinalo, Fenderter; FitzHugh, Will; Calvo, Sarah; Engels, Reinhard; Smirnuv, Serde; Atnoon, Deven; Brown, Adam; Allen, Nicole; Naylor, Jerome; Stange-Thomann, Nicole; DeArellanc, Kurt; Johnson, Robin; Linton, Lauren; McEwan, Paul; McKernan, Kevin; Talamas, Jessica; Tirrell, Andrea; Ye, Wenduan; Zimmer, Andrew; Barber, Robert D.; Cann, Isaac; Graham, David E.; Grahame, David A.; Guss, Adam M.; Sedderich, Reiner; Ingram-Smith, Cheryl; Kuettner, H. Graig; Kroycki, Joseph A.; Leigh, John A.; Li, Weiki; Liu, Jinfeng; Mukhopadhyay, Biswarup; Reeve, John M.; Smith, Kerry; Springer, Timothy A.; Umayam, Lowell A.; White, Owen; White, Robert H.; de Macario, Everly Conway; Ferry, James G.; Jarrell, Ken F.; Jing, Hua; Macario, Alberto J. L.; Paulsen, Tan; Pritchett, Matthew; Sowers, Metin P.; Swanson, Potald U.; Sinder, Steven H.; Dander, Error Not halt, William W.; Princet, B 2 12 2 4-

CORPORATE SOURCE:

Whitehead Institute Mater for Beaume Besearch,

Cambridge, MA, 00141, USA

SOURCE: Genome Research (2002), 12(4), 532-542

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal

DOCUMENT TYPE: Journal LANGUAGE: English

Methanogenesis, the biol. prodn. of methane, plays a pivotal role in the global carbon cycle and contributes significantly to global warming. The majority of methane in nature is derived from acetate. The complete genome sequence of an acetate-utilizing methanogen, Methanosarcina acetivorans C2A, is now reported. Methanosarcineae are the most metabolically diverse methanogens, thrive in a broad range of environments, and are unique among the Archaea in forming complex multicellular structures. This diversity is reflected in the genome of M. acetivorans. At 5,751,492 base pairs it is by far the largest known archaeal genome. The 4024 open leading tranes of is for a brittingly wide and unanticipated variety of metabolic and cellular capabilities. The presence of novel methyltransferases indicates the likelihood or undiscovered natural energy sources for methanogenesis, whereas the presence of single-subunit carbon monoxide dehydrogenases raises the possibility of nonmethanogenic growth. Although motility has not been obsd. in any Methanosarcineae, a flagellin gene cluster and two complete chemotamis gene clusters were identified. The availability of genetic methods, coupled with its physical and metabolic diversity, makes M. acetivorans a powerful model organism for the study of archaeal biol. The genome sequence is deposited in GenBank under Accession No. AE010656-AE011189.

T 406874-66-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Piclogical study)

(amino acid sequence; complete genome sequence of Methanosardina adetivorans 78A reveals extensive metabolic and physiol. diversity)

REFFRENCE 3 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 6 OF 26 HOAFLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:280980 HOAFLUS

DOCUMENT NUMBER: 137:18844

TITLE: Functional annotation of a full-length Analogysis

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Muramatsu, Masami; Hayashizaki, Yoshihide; Kawai, Jun; Carninci, Fiero; Itoh, Masayoshi; Ishii, Yoshiyuki; Arakawa, Takasiro; Shibara, Kasuhiro; Chinagawa, Akira; Shinopaki, Kabup Flant Matarila Emploration Team, Plant Functional CORFORATE COURTE: Senomios Res. Group, FIREN Jenomi variences Center GSC , Helel Kryadai, Ismaira, B Ee Jak, Jakan Science Washington, 10, United States, 1012, 196,88681, 141-148 nodem: colfac; lock: . ..-- 'F American Association : The Advancement of Clience PUBLISHER: TOOTHER THE . armal English AB Full-length cDNAs are essential for the correct annotation of genemic sequences and for the functional anal. of genes and their products. About 155,144 RIKEN Arabidopsis full-length (RAFL) aDNA clones were isolated. The 3'-end expressed sequence tags (ESTs) of 155,144 RAFL cDNAs were clustered into 14,668 nonredundant cDNA groups, about 60 of predicted genes. E'-ESTs were also obtained from 14,034 nonredundant cDNA groups and a promoter database constructed. The sequence database of the RAFL gonAs is useful for promoter anal. and correct annotation of predicted transcription units and gene products. Furthermore, the full-length cDNAs are useful resources for analyses of the expression profiles, functions, and structures of plant proteins. [This abstr. record is one of sixteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]. 437141-30-5 ΙT RI: BSU (Biological study, unclassified); PAP Properties ; PI L Pinininging Cotton (amino acid sequence; juncti nai annotation of a full-length Arabidopsis of NA collection; REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT L11 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2003 ACS 2002:173787 HOAPLUS 136:351357 Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; INVENTOR(S): Rank, David E. Molecular Dynamics, Inc., USA PATENT ASSIGNEE(S): PCT Int. Appl., 659 pp. SOURCE: CODEN: FINNEL DOCUMENT TYPE: Fatent English FAMILY ACC. NUM. COUNT: 84 PATENT INFORMATION: KINT DATE PATENT NO. W: AE, AG, AL, AM, AT, AY, AG, BA, BB, BB, BB, BY, BD, CA, CH, CN, OB, TH, TO, DE, DK, DM, ID, EE, ES, EI, GB, GI, GE, E, GM, HR, ID, II, IN, IS, JP, ME, KG, KF, KR, KJ, LC, LK, LR, LS, LT, IC, IC, MA, ME, MG, MK, MM, MM, MM, MZ, NO, MZ, FL, FT, RO, RU, SD, SE, SS, SI, SK, SL, TJ, TM, TR, TT, TZ, TA, TG, US, UZ, VN, TO, DA, DM, AM, AD, BY, KB, KD, MD, RU, TJ, TM

DE, DK, ES, FI, FR, GR, GR, IE, II, LU, MO, NL, FT, SE, TR, BF,

EM: GH, GM, KE, 18, MM, MD, SD, SL, SD, TZ, UG, EW, AT, FE, CH, CY,

BI, OF, DB, DI, DM, GA, PM, GW, ML, MR, ME, SM, TD, TB

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    W 01:010:07:07
    A2 20:010:40:8

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        ts 2010-632366 A 20000813
                                                                      TS 2000-234687P P 20000921
                                                                      US 2000-236359P P 20000927
                                                                      GB 2000-24263 A 20001004
                                                                      WO 2001-US664 A 20010130
       A single exon nucleic acid microarray comprising 13,109 single exon
        nucleic acid probes for measuring gene expression in a sample derived from
         human adult liver is described. These unique exons are within longer
         probe sequences; sequencing confirms the exact chem. structure of each
         probe. Some amplicons have more than one exon, and some exons are
         contained in more than one amplicon. Expression, homol., and functional
         information are provided for the genome-derived single exon probes that
         are expressed significantly in human adult liver cells. Also described
         are 12,886 single exon nucleic acid probes and 12,583 proteins expressed
         in the adult liver and their use in methods for detecting gene expression.
         The genome-derived single exch nucleic acids comprise a novel type of
         nucleic acid microarray for verifying sene empression. In a man, bothers
         are provided for identitying exchange as a element to be be, as a con-
        assigning exens to a single dene.
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        420924-39-6
        RI: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological
        use, unclassified); PRP (Properties); ANST (Analytical study); BIOL
         (Biological study); USES (Uses)
         (amino acid sequence; human genome-derived single exon nucleic acid
              probes useful for anal. of gene empression in human adult liver)
L11 ANSWER & OF 26 HUAFLUS COPYRIGHT 2003 ADS
                                            2002:157787 HCAPLUS
DOCUMENT NUMBER:
                                            136:195341
TITLE:
                                            Cloning and cDNA and deduced amino acid sequences of
                                            21 human secreted proteins
INVENTOR(S):
                                           Rosen, Craig A.; Komatsoulis, George A.; Baker, Kevin
                                            P.; Birse, Charles E.; Soppet, Daniel E.; Olsen,
                                           Henrik S.; Moore, Faul A.; Wei, Fing; Fbner, Reinhard;
                                            Turn, C. Busting; Chi, Yangar, the L, His Bis wills,
                                            Mi thele; Ni, Jian
                                           Human Jenome Shiennes, Inc., USA
PATENT ASSIGNEE (S):
SOURCE:
                                           FCT Int. Appl., 134 pp.
                                            DOCUMENT TYPE:
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FAMILY ACC. NUM. CONT:
PRINT INFORMATION:
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    WO WI 2016991 AI WI 20121226 W UT 1-001476 U 1 110
        N: AE, AB, AL, AE, AT, AT, AC, BA, BB, BB, BB, BB, BC, BC, BC, BC,
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            BI, OF, OG, OI, OM, GA, OM, WW, MI, MR, ME, OM, TI, TG
    PRIORITY APPIN. THEO.:
                                    W0 2001-US1435 W 2001
   The present invention relates to 21 novel human secreted proteins and
AB
    isolated nucleic acids conty. the coding regions of the genes encoding
    such proteins. Tissue distribution, sequence homologies, and preferred
    epitope sites are provided for the secreted proteins, as well as
    chromosomal mapping of some of the genes. Also provided are vectors, host
    cells, antibodies, and recombinant methods for producing human secreted
    proteins in barterial, insect, and mammalian velle. The invention further
    relates to diagnostic and therapeutic methods userul for diagnosing and
    treating disorders related to these novel human segreted profeins.
    High-throughput screening assays are also provided for various putative
    activities of the secreted proteins.
    400696-91-5P
    RL: BFN (Biosynthetic preparation); BST (Biological study, unclassified);
    PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP
     (Preparation); USES (Uses)
       (amino abid sequence; bloning and bLNA and deduced amino abid sequences
       of 21 human secreted proteins)
REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS
                            RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L11 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:125123 HCAPLUS
DOCUMENT NUMBER
                      130:145954
                      Genome sequence of the plant pathogen Raistonia
                      solanabearum
AUTHOR(S):
                      Salanoubat, M.; Genin, S.; Artiguenave, F.; Gouzy, J.;
                      Mangenot, S.; Ariat, M.; Billault, A.; Brottier, P.;
                      Camus, J. C.; Cattolico, L.; Chandler, M.; Choisne,
                      N.; Claudel-Renard, C.; Cunnac, S.; Demange, N.;
                      Gaspin, C.; Lavie, M.; Moisan, A.; Robert, C.; Saurin,
                      W.; Schiew, T.; Siduler, P.; Thebault, P.; Whalen, M.;
                      Wincker, F.; Serry, M.; Weichener H., J.; Bolder, A.
                      CORECRATE SCURTE:
                      Nature Timesh, United Hingdon (21 2 , 411) to 11,
SOTRIE:
                      497-500
                      CODEN: MATURS; ISSN: 0029-0836
FUBLISHER:
                      Nature Publishing Group
                      Journal
DOCUMENT TYPE:
LANGUAGE:
                      English
   Ralstonia solanacearum is a devastating, soil-borne plant pathogen with a
AB
    plobal distribution and an unusually wide host range. It is a model
    system in the dissection of mol. Weterminants governing rathesemicity.
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AB Raistonia solanadearum is a devastating, soil-borne plant pathogen with a global distribution and an unusually wide host range. It is a model system to the itesection of mol. Noterninants governing pathogenicity. The complete genome sequence and its anal. of strain CMIICO is presented. The E.S-medabase (Mb) genome is organized into two replicons: a 3.7-Mb chromosome and a 2.1-Mb medaplasmid. Both replicons have a mosaic structure providing evidence for the adquisition of genes through horizontal gene transfer. Regions conty, genetically mobile elements assocd, with the percentage of 3.0 bias may have an important function in genome evolution. The senome encoles many protection provided associal with a role in pathogenicity. In particular, many protection of a content.

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lactors were identified. The complete repertoire of type III secreted effector proteins can be studied. Over 40 candidates were identified. Comparison with other genomes suggests that bacterial plant pathogens and animal mathemens harbor distinct armays of specialized type [III-dependent leti≣e ttobbe.

394342-70-2 394342-96-2

RL: ESU (Biological study, unclassified ; FRE (Properties); HIOL [Hiclogical study]

(amino acid sequence; genome sequence of the plant pathogen Ralstonia solanacearum)

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RESCORD. ALL CITATIONS AVAILABLE IN THE RE FRANCE

111 AUGMER I. File BIRLING CHIRLING CA. ACCHOSION NUMBER: AND ACCEPTAGE AND ACCEPTAG

130:227573

TITLE: Human genome-derived single exon nucleic acid probes

useful for analysis of gene empression in human

placenta

INVENTOR (S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

Rank, David R.

PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA

POT Int. Appl., 654 pp. SOTROE:

-CODEN: PIXMD2

DOCUMENT TYPE: Patent English LANGUAGE:

FAMILY ACC. NUM. COUNT: 84

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     WO 2001057272 A2 20010509 WO 2001-MF603 AU 10150
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A single emon nubleid abia mibroarray our risina 13,030 single emon. _____ nucleic acid probes for measurin; dene expression in a sample derived from human placenta cells is decomber. These unique em na are within I nger prote sequences; so pending whitens the examples. Should be a build raike. Is no mailining have note in the one of the contract of the contained in more than one amplicant. Empression, number, and functional information are provided for the genome-derived single exon probes that are expressed significantly in human placenta. Also described are 13,000 single exch nucleic acid probes and 12,605 proteins expressed in the placenta cells and their use in methods for detecting gene empression. The genome-derived single exch nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exchs to a single gene. (This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the accument and publication system constraints.].

IT 400664-75-7

FL: AMT (Analyte); BSU (Biological study, unclassified); PRP (Properties); AMST (Analytical study); BIOL (Biological study)

(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human placency

111 AMSWER 11 OF LA HOAFLYD OUFFRIGHT WORK AND

ACCESSION NUMBER: 2002:1106 6 HOAPLY.

DOCUMENT NUMBER: 138:198268

TITLE: Human genome-derived single exon nucleic acid probes

useful for analysis of gene empression in human fetal

liver

INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

Rank, David R.

PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA

SOURCE: FOT Int. Appl., 639 pp.

CODEN: PINND2

DOGUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 84

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             DE, 18, EC, EI, EF, E, OF, IE, II, II, MO, MI, ET, SE, TF, EF,
             BJ, GF, GB, GI, GM, GA, GN, GM, MI, MR, ME, GN, TI, TG
     PRIORITY APPLIA. INT. .:
                                         TS 2000-180312F F 20000204
                                         MS 2000-200456P F 2000526
                                         TS 2000-608408 A 20000630
                                         tis 2010-632366 A 20061863
                                         T3 2010-03465TP F 20000921
T3 2010-23465TP F 20000921
T3 2010-23485TP F 20000921
T3 2010-23485TP F 20000920
T3 2010-23485TP F 20000920
T3 2010-23485TP F 20000920
    A single ewon nucleic acid mirroarray comprising 10,000 single ewon
AΒ
     nucleic acid probes for measuring gene empression in a sample derived from
     human fetal liver cells is described. These unique emons are within
     langer probe sequences; sequencing annima the exect diem. structure of
     each probe. Some amplicons have more than one emon, and some emons are
     contained in more than one ampliann. Expression, how C., and functional
     information are provided for the sen me-derived single exem probes that
     are emplessed significantly in human istal liner colus. Also described
     are 12,456 single exon nucleic acid probes and 12,027 proteins expressed
     in the fetal liver and their use in methods for detecting gene expression.
     The genome-derived single exon nucleic acids comprise a novel type of
     nucleic acid microarray for verifying gene expression. In addr., methods
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required to fully indem the document and publication system constraints.]. IT 400957-73-5

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)

records for this document necessitated by the large no. of index entries

(amino acid sequence; human genome-derived single emon nucleic acid probes useful for anal. of gene empression in human fetal liver)

L11 ANSWER 13 OF 26 HORPLUS COPYRIGHT 1004 AGS ACCESSION NUMBER: 10 2:11 540 HOAPLUS

DOCUMENT NUMBER: 150:000 2

TITLE: Human genome-derived single extra numbers avid probes useful for analysis of gene expression in human brain

are provided for identifying exons in a eukaryotic genome, and for

assigning exons to a single gene. [This abstr. record is one of nine

INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

Rank, David R.

PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA

SOURCE: POT Int. Appl., 650 pp.

CODEN: PINNED

DOGUMENT TYPE: Parent LANGUAGE: English

FRMILE ACC. NUM. COUNT: 84

PAT	IENT	NO.		KI	V2	DATE			A	PPLI	CATI	ON N	Э.	DATE			
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	BW:	11, 11, 15,	22, 22, 28, 23,	28, 22, 23,		AC, XX, Eb, SA,	F1, E2, E4,	E3, 21, 28,	- ::, - :::,	32, 32, 32,	~ · · · /		,		BE,	011, Th,	7. X ,
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GB 2361238
                     EW: GH, GM, KE, LS, MM, MZ, SD, SL, SZ, TD, UG, ZM, AT, BE, CH, CY,
      DE, DK, ES, FI, FR, BE, BR, IE, II, LU, MO, MI, FT, SE, TF, BE,
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  PRIORITY APPLN. INFO.:
                   US 2000-207456P P 20000526
                    US 2000-608408 A 20000630
                   US 2000-632366 A 20000803
                   US 2000-234697P P 20000921
                    US 2000-236359P P 20000927
OB 2000-24263 A 20001074
```

A single exon nucleic acid microarray comprising 12,821 single exon AB nucleic acid probes for measuring gene expression in a sample derived from human brain cells is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exch, and some exchs are contained in more than one ampliann. Empression, homel., and functional information are provided for the genume-derived single exch probes that are empressed significantly in human brain. Also described are 12,613 single exon nucleic acid probes and 11,377 proteins expressed in the brain and their use in methods for detecting gene empression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exens to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints. [.

1T 412969-90-5

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study) (amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human brain)

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ACCESSION NUMBER:
DOCUMENT NUMBER:
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                         useful for analysis of year empression in human bone
                         marrow
INVENTOR(S':
                         Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;
                         Rank, David R.
FATENT ASSIGNEE (S):
                         Molecular Dynamics, Inc., USA
                         POT int. Appl., elipp.
SOURCE:
                         CODEN: FIREC
IAURUARE:
                         Eryllish
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:
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TAX 200101727		Wind Indian Harris	

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             CR, CU, CO, LE, DK, LM, CO, EE, ES, FI, GB, GO, GE, GH, GM, HR,
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     GH 2360284 A1 | 20010913 | GH 2000-24286 | 2001054
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         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
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            BI, OF, OG, OI, OM, GR, GN, GN, MI, MR, NE, SN, TD, TG
     TB 200217/252 AI 2002 BO TB 2001-827998 20016408
PRICRITY APPLN. INFO.:
                                      US 2000-180312F P 20000204
                                      US 2000-207456P P 20000526
                                      US 2000-608408 A 20000630
                                      US 2000-632366 A 20000803
                                      US 2000-234687P P 20000921
                                      US 2000-236359P P 20000927
                                      GB 2000-24263 A 20001004
                                      WO 0001-US669
    A single exon nucleic acid microarray comprising 10,114 single exon
AB
    nucleic acid probes for measuring gene empression in a sample derived from
     human bone marrow is described. These unique extra are within longer
    probe sequences; sequencing confirms the exact chem. structure of each
    probe. Some amplicons have more than one exon, and some exons are
    contained in more than one amplican. Expression, homol., and functional
    information are provided for the genema-derived single examprobes that
    are expressed significantly in human bone marrow. Also described are
     12,898 single exon nucleic acid probes and 12,616 proteins empressed in
    the bone marrow and their use in methods for detecting gene empression.
    The genome-derived single exon nucleic acids comprise a novel type of
    nualeia adid microarray for verifying gene expression. In addn., methods
    are provided for identifying exons in a eukaryotic genome, and for
    assigning exchs to a single gene. [This abstr. record is one of nine
    records for this document necessitated by the large no. of index entries
    required to fully index the document and publication system constraints.].
    402671-83-4
    RL: ANT (Amalyte); BST (Biological study, unclassified; PSF (Properties); AMST (Amalytical study); BICL (Biological study)
       (amino acid sequence; human genome-derived single ewon nucleic acid
       probes useful for anal. of gene expression in human bone marrow)
111 ANSWER 14 OF 26 ETABLIS COPPRISED 2 - ASS
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                      Brsen, India A.; Barash, Steven J.; Ruben, Steven M.
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FATENT ASSIGNEE G : Humano Manora Calendary, Inc., NUA FILE FIRMLE

DOCUMENT TYPE:

Patent

LANGUAGE: Eng FAMILY ACC. MWM. COMMT: PA PATEMI IMPOPMATION:

FATENT NO.		APPITATI N N . TATA	
W3 2001156367 W: AE, AG, CR, CU, HT, IC, LU, LY, SD, SE, YU, ZA,	A1 A1.11 a A1, AM, AT, A0, DZ, DE, DK, DM, IL, DM, DS, DB, MA, MD, MG, MK, SG, SI, SK, SL, ZW, AM, AZ, BY,	N	11 7A, 7E, 7M, GH, GM, HR, LR, LS, LT, PT, RO, RU, TS, UZ, VM,
EW: GH, GM, DE, DK, BF, CF, AU 2001041413 AU 2001041417 AU 2001050770 US 2002042096 US 200206821 US 200206821 US 200206821 US 200206823 US 200216102638 US 200216102638 US 2002161479 US 2002161208 US 2002161208 US 2002163454 EP 1261703	KE, LS, MW, MZ, ES, FI, FR, GB, GG, GI, GG, GA, AB 20010807 AB 20010807 AB 20020411 AB 20020620 AI 20020704 AI 20020711 AI 20020711 AI 20020711 AI 20020713 AI 20020714 AI 20020715 AI 20020711 AI 20020712 AI 20020713 AI 20021010 AI 20021017 AI 20021017 AI 20021021 AI 20021021 AI 20021121 AI 20021204	SD, SI, SZ, TZ, TG, ZW, AT, GH, IE, IT, IM, MM, ML, FT, AM, MM, MM, MM, TM, AM, AM, AM, AM, AM, AM, AM, AM, AM, A	117 117 117 117 117 117 117 117 117 117
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US 2000-256719P P 20001205
US 2000-251479P P 20001206
US 2000-251856P P 20001208
US 2000-251868P P 10001208
US 2000-251869P P .20001208
US 2000-251990P P 20001208
US 2001-764863 B1 20010117
WO 2001-US1338 W 20010117
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The present invention relates to novel musculoskeletal system-related AΒ polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "musculoskeletal system antigens", and the use of such musculoskeletal system antigens for detecting disorders of the musculoskeletal system, particularly the presence of cancer and cancer metastases. More specifically, 1023 isolated musculoskeletal system-assocd. cDNA mols. are provided encoding noval musculoskeletal system-assocd. polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system assocd. polynuclectides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

ΙT 384873-95-4P

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); FRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

[amino acid sequence; human musculoskeletal system-specific nucleic acids and their encoded proteins and antibodies)

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L11 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                        2001:763025 HCAPLUS
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195:335111 DOCUMENT NUMBER:

Albumin fusion proteins with therapeutic proteins for TITLE:

improved shelf-life

INVENTOR(S): Rosen, Oralg A.; Haseltino, William A.

PATENT ASSIGNED (8%: Human Genome Onion way, Inc., DOR.

FOT Int. Appl., 1992 pp. SOURCE:

CODEN: FINND2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT:

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             DE, DK, ES, FI, FR, GB, GR, IE, II, LU, MC, ML, PT, SE, TR, BF,
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     EP 1200086 A1 20080122 EP 2001-944114 20010412

E: AT, BE, CH, DE, DK, ES, FF, GE, GE, IT, LI, LU, ML, SE, MC, FT,
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FRIORITY ARRIVE THREE.:
                                         TO 2000-229305P F 20000412
TO 2000-199384P F 20000425
                                         MS 2000-250931P P 20001221
                                         W0 2001-7811955 W 20010412
    The present invention encompasses fusion proteins of albumin with various
A =
     therapeutic profeins. Therapeutic proteins may be stabilized to extend
     the shell-life, and/or to retain the therapeutic protein's activity for
     extended periods of time in solm., in with an ion in viv., by which sally
     or ther. Easing the configuration the therapeating of them to all more than
     fragment or variant of allowing the factors is a protein bay also
     reduce the need to formulate the protein solns, with large excesses of
     carrier proteins to prevent loss of therapeutic proteins due to factors
     such as binding to the container. Nucleic acid mols. encoding the albumin
     fusion proteins of the invention are also encompassed by the invention, as
     are vectors contg. these nucleic acids, host cells transformed with these
     nucleic acids vectors, and methods of making the albumin fusion proteins
     of the invention and using these nucleic acids, vectors, and/or host
     bells. Thus, plasmid weathers are constructed in which DNA encoding the
     desired therapautic protein may be inserted for expression of the albumin
     fusion proteins in yeast (pPPC0005) and mammalian cells (pC4:HSA).
     Yeast-derived signal sequences from Saccharomyces cerevisiae invertase
     SUC2 gene, or the stanniocalcin or native human serum albumin signal
     peptides, are used for secretion in yeast or mammalian systems, resp.
     Thus, the fusion product of human growth hormone with residues 1-387 of
     human serum albumin retains essentially intact biol. activity after 5 wk
     of incubation in tissue culture media at 37.degree., whereas recombinant
     human growth horm he used as control list its bid. A wintry in the first
     week. Although the potenty of the alkumin rusi a protected is signifi-
     lower than the unjused counterparts in rapid bloassays, their bull.
     stability results in much higher biol. activity in the longer term in
     vitro assay or in vivo assays. Addnl., the present invention encompasses
     pharmaceutical compns. comprising albumin fusion proteins and methods of
     treating, preventing, or ameliorating diseases, disorders or conditions
     using albumin fusion proteins of the invention.
     369644-05-3
     RL: FRE (Properties
        (unclaimed protein sequence; albumin fusion proteins with therapeutic
        proteins for improved shelf-life)
REFERENCE COUNT:
                               THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L11 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                         2001:582028 HOAPLUS
TOTMENT NUMBER:
                         136:163431
                         Mublein abids and their enorded polypertides from
                         finan kana marraw
INVENTOR S':
                         Fond, John E.; Poyle, Pryan J.; Tana, Y. Ton; Illu,
                         Chenghua; Asundi, Timoi, Thou, Fing; Yue, Alimby J.;
                         Ren, Feliyan; Demanas, Faille T.
PATRIT RECENTE C':
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PRIORITY APPLN. INFO.:
                                   US 2000-598075 A 20000620
                                    US 2000-020325 A 20000719
                                    US 2000-250583P A 20001130
                                    WO 2001-US3782 W 20010268
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The present invention provides a dellection or library of 94 nucleic acid AΒ contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The SDNA libraries are from human bone marrow sources and nearest neighbor sequence himslyies are provided. The invention also relates to the proteins environ by sitting lynamie thes, along with therapeutic, diagnost. Then a research under this icr therepolynucleotides and proteins.

353568-97-5 354113-34-1

RL: ANT (Analyte); BOS (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(amino acid sequence; nucleic acids and their encoded polypeptides from human bone marrow'

111 ANSWER 17 OF 26 HOAFLUS COPYRIGHT 2003 ACS

2001:566854 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 135:163414

TITLE: Human nucleic acids and their encoded proteins and

antibodies

INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.

PATENT ASSIGNED S': Human Genome Solences, Inc., USA

SOURCE: FOT Int. Appl., 532 pp.

NIEW: Firm.

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ADD. NUM. COUNT:

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PRIGRITY APPIN. INFO.:
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                W ..0010117
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The present invention relates to novel human polynucleotides and the polypeptides encoded by these polynucleotides, and the use of such polypeptides for detecting disorders. More specifically, "9 isolated human cDNA mols, are provided encoding novel polypeptides. Antibodies that bind to these polypeptides are also provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing the novel human polynuclectides and/or polypeptides. The invention further relates to diagnostic and therepouted mathods useful for diagnosing, treating, preventing and or prognosing distributes and therapeutic methods for treating such discretes. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compr.s. for inhibiting the grodn, and function of the polypeptides of the present invention.

IT 353554-69-5, Protein (human clone HFIEC13)

RL: BSU (Biological study, unclassified); PFP (Properties); BIOL (Biological study)

protein sequences; human nucleic acids and their encoded proteins and antibodies'

REFERENCE COUNT:

THERE ARE C CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

LII ANSWER 18 OF 26 HOAFLUS COFYRIGHT 2003 ACS ACCESSION NUMBER: 2001:397089 HOAFLUS DOCUMENT NUMBER: 138:29431

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 INVENTOR S :
                                          Lerchl, Jens; Rend, Andreas; Ehrhardt, Thomas; Reindl,
                                          Andreas; Cirpus, Fetra; Bischoff, Friedrich; Frank,
                                          Markus; Frenci, Anerte; Duwenia, Elke; Schmidt,
                                          Ralf-Michael: Beecht, Ralf
                                       Basi Flant delende Umbh, Germany
 SOURCE:
                                         FOI Int. Appl., 113 pp.
                                         CODEN: PINNIC
 DOCUMENT TYPE:
                                          Patent
                                          English
 FAMILY ACC. MMM. MMMT:
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         WO 2001038841 A1 20010881
                                                                       WU 1999-EP9105 19991125
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PRIORITY APPLN. INFO.:
                                                                  WO 1999-EP9108 W 19991125
                                                                   WO 2000-EP11615 W 20001122
        Isolated numbers acid mols., designated LMRP numbers and mols., which
AB
        endodo novel IMREs from e.g. Physonicialla patents are described. The
         invention also provides antisense nucleid adid mols., recombinant
        expression vectors contg. LMRF nucleic acid mols., and host cells into
        which the expression vectors have been introduced. The invention sill
         further provides isolated LMRPs, mutated LMRPs, fusion proteins, antigenic
        peptides and methods for the improvement of the prodn. of a desired compd.
        from transformed cells, organisms or plants based on genetic engineering
        of LMRP genes in these organisms.
        343286-49-7
        RL: BUU (Biological use, unclassitied); FRF (Properties); Bith (Hiological
        study); USES (Uses)
              (amino arid sequence; genes of Physromitrella patens enroding homolous
             of enzymes of synthesis of polymosatd. fatty acids and lipids'
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REFERENCE COUNT:
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ACCESCION NOTHER:
Decomposition of the second
                                        Sequence-distrimined DNA fragments and corresponding
                                         encoded polypeptides from corn and Arabidopsis
INVENTOR(S):
                                         Alexandrov, Mickelai; Brover, Vyacheslav; Chen,
                                         Mianfend; Subramanian, Gopalakrishnan; Troukhan, Mawim
                                         E.; Cheng, Liansheng; Dumas, J.
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FATEUT ADDI NEED : Needes Inc., TOA Eur. Fat. Aggl., DOOMENT THE: Patent LANGUAGE: Engl FAMILY ACO. NOW. CONT: 10 FAIFUT INFORMATION:

FATENT NO. MINU TATE AFFILTMENT NO. DATE A2 20000906 EF 1033400 EP 2000-301439 20000225 F: AT, BE, CB, CE, CK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, FT, IE, SI, LT, LV, FI, RO TE, SI, LT, LV, FI, RO A2 20001122 EP 1054000 EP 2010-304161 20000517 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, ML, SE, MC, PT, IE, 31, LT, LT, F1, R0 PRIORITY AFELM. IMPO.: 73 1949-101825P P 1999022c 73 1999-145918F E 19940727 UR 1922-1474515 B 14245505 70 1449-140355F F 18980802 US 1999-146389P P 19990802 US 1999-147038P P 19990803 US 1999-147204P P 19990804

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TS 1999-134213F P 19990514
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The present invention provides DNA mols, that constitute fragments of the AB genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA nols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis ENA is used in the present expt., but the procedure is a general one. Frotocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA13316218528Q necessitated by the large no. of index entries required to fully index the document and publication system constraints.]. IT

302645-65-4 302645-66-5

FL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); CCCU (Occurrence); USES (Uses)

(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

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L11 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                       2000:754707 HCAPLUS
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DOCUMENT NUMBER:

133:318296

Sequence-determined DNA fragments and corresponding TITLE:

encoded polypeptides from corn and Arabidopsis INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen,

Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim

E.; Zheng, Liansheng; Dumas, J.

Ceres Inc., USA PATENT ASSIGNEE(S):

Eur. Pat. Appl., 339 pp. SOURCE:

CODEN: EPNXDW

DOCUMENT TYPE: Pater LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1.6

PATENT NO.	KIND DATE	AFFLICATION NO.	DATE
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DD 1999-138194B P 199908 9 The present invention provides DNA mols, that constitute fragments of the genome and collas from Cea mays mays HYPRID SEED #35Als and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides endo by thereby. The DNA mole. The sector for exectifying a second product in cells, within as a promoter or as a protein solding sequence or as an MTE of as a st termination of terms, our are such a structured by the contraction of the game in the one mistre, in our cline the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DMA is used in the present empt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CATHOLOGICA, hopewait studing the large no. of index entries required to fully index the accument and publication system constraints.). 302411-42-3 302411-43-4 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); FRF (Properties); BIOL (Biological study); OCCU (Codurrence); USES (Uses amino adia sequence; sequence-deta. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis) i (lako inden 1907)

111 ANSWER 21 OF 26 HOAPLUS COPYRIGHT 1 18 ACS 139:30638 Sequence-determined DNA fragments and corresponding TITLE: encoded polypeptides from form and Arabidopsis INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Mianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J. PATENT ASSIGNEE(S): Ceres Inc., USA Eur. Pat. Appl., 339 pp. SOURCE: CODEN: EPHMOW DoctRENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16

FATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE EP 1033405 A2 00000908 R: AT, BE, CH, EE, DK, ES, FR, GP, GR, IT, LI, LU, NL, SE, MC, PI, CA 2000-1300692 | D0000225 AA 200003825 CA 2300692 CA 2302828 EP 1055728 **.** R: AT, BE, CH, CH, CK, ES, BR, GR, GR, IT, LI, LU, NL, SE, MC, ET, IE, SI, IT, IN, FI, BO ha lacconia EE 2010-814161 20000817 R: AT, BE, CH, CE, CK, EC, FR, CH, CR, III, LI, LI, SE, KI, FI, 1E, S1, LT, 17, F1, B3 PRICRITY APPLM. INFO.: TS 1999-121-25F F 18990225 US 1999-145919P P 19990727 US 1999-145951P F 19990728 US 1999-146396P US 1989-146398P US 1999-146389E 19990802 TS 1999-147738E 1000000000 12 1484-1471349 19997874 US 1999-147192P E US 1949-1471001E F 19991918

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US 1999-132863P P 19990507
US 1999-134256P P 19990511
US 1999-134218P P 19990514
US 1999-134219P
                                            P 19990514
US 1999-134221P
                                            -P 19990514
US 1999-134370P
                                           P 19990514
US 1888-134768E
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US 1999-134941P P
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US 1999-135124P P 19990520
US 1999-135353P P 19990521
US 1999-135629P P 19990524
US 1999-136021P
                                             P 19990525
US 1999-136392P P 19990527
US 1999-136782P P 19990508
US 1999-137222P P 19990601
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US 1999-1307902P E
US 1999-130724F E
                                                     12931604
                                                    1999.6.7
US 1999-138094P P 19990608
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The present invention provides DNA mols, that constitute fragments of the ABgenome and cDNAs from Lea mays mays (HYPRID SEED #38Al9) and Arabidopsis thaliana (ecotype Wassilewski', and polypeptides enough) thereby. The DNA mols, are useful for specifying a mene product in cells, either as a promoter or as a protein hoding sequence or as an UTB or as a se bermination sequence, and are also useful in controlling the behavior of a Tene in the chromosome, in controlling the empression of a gene or as tools for genetic mapping, recognizing or isolating identical or related TNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis INA is used in the present empt., but the pricedure is a general one. Frotogola are provided for Southern hybridications and transformation of parrot della. [This abstr. repord is one of 18 records supplemental to CA1331621: Luty necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

301564-26-1 301564-27-2

RL: BOC (Biological obcurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BRP (Properties); BIOL (Biological study); COCU (Courrence); USES (Uses)

amino abid sequence; sequence-detd. DNA fragments and corresponding enouged polypertides from corn and Arabidopsis;

HII ANSWER 22 OF LC HOAPLUS COPYFIGHT 2013 AND

COBSGION NUMBER: UIII: 80-010 ECREDO

DUCTMENT NUMBER: 134:24" :

TITLE: Cloning and empression of a gene encoding a suparity

chloroplast .one park latty a dia desaturake .f marine

Chlampann has

AUTHOR(8): Miyasaka, Hitoshi; Tanaka, Santshi; Kanah shi, Harus

CORPORATE SOURCE: Tech. Bes. Cent., The Kunsai Electric Bower 1., 11-0

Makoji -- onume, Amajasaki, Hyla, , , /l-14/4, Yagan SOURCE: Flant Fisha Hindley Trayo - 2, , 17 1 , 147-171

001EN: 018188; 100N: 1342-408

PUBLISHER: Japanese Society for Plant Cell and Molecular Biology

DOCUMENT TYPE: Journal LANGUAGE: English

AB A cDNA encoding putative chloroplast .omega.6 fatty acid desaturase was isolated from a cDNA library of marine Chlamydomonas sp. strain W-80. The mRNA level of this gene under various conditions of stress was examd. by northern plotting anal., and the transcript level was increased under a cold-stressed [4.degree.] condition.

II 307998-10-3

RL: PRP (Properties)

(amino acid sequence; cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomonas)

L11 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2:03 ACS

ACCESSION NUMBER: 1998:773005 HOAFLUS

DOCUMENT NUMBER: 181:18 - 34

TITLE: Deciphering the bill gy of My regovernum tower oulosis

from the complete genome sequence. (Erratum to

document dited in CA129:77224]

AUTHOR(S): Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.;

Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier, K.; Gas, S.; Barry, C. E., III; Tekaia, F.; Badcock, R.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, E.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.; Helreyi, S.; Hornsby, T.; Jagels, K.;

Hrogh, A.; Molean, J.; Moule, S.; Murphy, L.; Oliver,
H.; Osborne, J.; Quail, M. A.; Rajandream, M.-A.;
Rogers, J.; Rutter, S.; Seeger, K.; Skelton, J.;

Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.

CORPORATE SOURCE: Sanger Cent., Wellcome Trust Genome Campus, Hinkton,

omani taka omki

SINURGE: Lature I have 1 + h + h + h + h + h + h + h

2025N: MANTAO; 180N: 15-15-1

FUBLISHER: Macmillan Majazin s

DOCUMENT TYPE: Cournal LANGUAGE: English

Table I was published with some symbols missing; the correct version can be found at http://www.sanjer.ac.uk/ani/is/diven/here. In Fig. 1, Fv064* was incorrectly labeled as fail 57 instead of fabou. Two of the genes for myorly! transferases were inverted: Fv 11.75 end declarified at the fail not sold of at i, who head buttoned is for the general protein MFTs! and not antiden +50 intect. Incomp. is, oil +10.0 lest; Fv+130 is now designated fbyD. The sequence of Fv174* from M. bovis BOG-Fasterr

presented in Fig. * : was inversely and an absence and in a least and deletion instead in the

208786-02-1

Al: FER Prinerales

deciphering the blil. If Myscharterium taker sulssis in notice summittee genome sequence (Erratum,)

111 ANDWER 24 OF 26 HOWELDS SUFFRIGHT 25 8 ADD

ACCESSION NUMBER: 1999:399008 HOAPING

lindrin ninger: 1.....

lenguaring the disligy of Mydobacterium tokerdulosis

from the complete genome sequence

RITHIN S : Oble, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier,

K.; Gas, S.; Barry, C. E., III.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor,

R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroya, S.; Hornsby, T.; Jagels, K.; Krosh, A.; Molean, I.; Mole, S.; Morghy, I.; Oliver, W.; Oshirme, J.; ,usil, M. A.; Bajandrod, M.-A.;

Rogers, J.; Rutter, J.; Seeger, K.; Skolton, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.;

Whitehead, S.; Barrell, B. G.

Sanger Cent., Well wme Trust Genome Campus, Hinmton, CORPORATE SOURCE:

CRIC ISA, UK

Nature (London) (1998), 393 6685), 537-844 CODEN: MATURS; ISSN: 1028-0836 SOURCE:

FUELISHER: Natmillan Madaziness

DOCUMENT TYPE: Journal LANGUAGE: English

Countless millions of people have died from tuberculosis, a chronic infectious disease caused by the tubercle bacillus. The complete genome sequence of the best-characterized strain of Mycobacterium tuberculosis, Horky, was detd. and analyzed in order to improve our understanding of the biol. of this slow-growing pathogen and to help the conception of new prophylactic and therapeutic interventions. The genome comprises 4,411,529 base pairs, contains around 4000 genes, and has a very high G+C content that is reflected in the biased amino acid content of the proteins. M. tuberculosis differs radically from other bacteria in that a very large portion of its coding capacity is devoted to the prodn. of enzymes involved in lipogenesis and lipolysis, and to 2 new families of glycine-rich proteins with a repetitive structure that may represent a source of antigenic variation.

208786-02-1

A Section of the sect

RI: PRI Properties

camino acid sequence; deciphering the fill. It Mystelds his

tuberculosis from the complete genome sequence

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 25 OF 26 HOAPLUS COPYRIGHT 2013 ACS

ACCESSION NUMBER: 1998:61353 HCAPLUS

DOCUMENT NUMBER: 125:214937

... To mind of a gene for diloroplast .cmega. / desaturase

or a green alga, Chlangiomonas reinhardtii

AUTHOR S : Sato, Norihiro; Fujiwara, Shoko; Kawaguchi, Akihiko;

Tsuzuki, Mikio

School of Life Science, Takya University of Fharmady CORPORATE POTROE:

ani life Science, Tokyo, 192-03, Japan

Trunnsl of Biochemistly Tokyo - 1947, 12, 7 ,

10 ED: 1 BIA: ; IDD: 0.1-6.4X of a processor Billions for the control of the state of

AB A gene for chloroplast .omega.6 desaturuse, which catalynes the desath. . : mendencie to diencie acids in chloroplasts, was isolated from Chlamydomonas reinhardtii. Reverse trank miptaket lymerake opan reaction was first performed with oliver home time forces. The common section is in the first of the interest of the product of the product of the first of the contract of the first of the f .DELTA.12 wesaturases in myanika mania, buing it relimanshil poly a e bMA. An amplifie & DNA fragment in 1.7 an, binty, a trame for a protein humulogous to these desaturases, was used as a prope for spreening oDNA and denomic DNA libraries of C. reinhardtii. The oDNA clone of 2.2 kb obtained contained an open reading frame encoding a protein of 424 amino apids with a putative mil. mass of 48.4 kDa, the amino apid sequence of which showed 46-81 (home), to those of higher plant plastid .omega.6 and ory incha oterial (IFLTA, 11 desaturases). Infroduction of the oloned denomin counterpart of this cDNA, designated as dese, into a Chianydomonas mutant with defects in chloroplast .cmega.6 desath. and in the activities of photosystems I and II (FSI and FSII) complemented the desath. mutation, indicating that the dese gene cides for chloroplast .omega.6 desaturase. The complemented strains did not recover from the photosynthetic lesions, but showed lower PSII activity at 45.degree. than the desath. mutant, proving that the photosynthetic lesions in hf-9 are not caused by the desath. mutation, and that the lowered unsath. level of chloroplast lipids in the mutant is responsible for the empression of this might become of FOIT activity, one of the thylakoid membrane functions.

IT 204279-00-5

RL: BSU (Biological study, unclassified; FRP (Properties); BIOL (Biological study)

(amino acid sequence; cloning and sequence of gene dese for chloroplast .omega.6 desaturase of a green alga, Chlamydomonas reinhardtii)

L11 ANSWER 26 OF 26 HOAPLUS COPYRIGHT 2013 ACS

ACCESSION NUMBER: 1998:938841 HOAPLUS

DOCUMENT NUMBER: 124:47157

TITLE: Identification and functional analysis of the transfer

region of plasmid pMEA300 of the methylotrophic

actinomycete Amycolatopsis methanolica

AUTHOR(S): Vrijbloed, J. W.; van der Put, N. M. J.; Dijkhuizen,

Τ..

CORFORATE SOUFOF: Dep. Microbiology, Univ. Groningen, Haren, 9751, Neth.

SOURCE: Journal of Bastéhiology (1995), 177 (22), 6499-505

CODEN: JOBAAY; ISSN: 0021-9193

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

Amydolatopsis methanolida dontains a 13.3-kb plasmid (pMRA300) that is AB present either as an integrated element or as an autonomously realizating plasmid. Conjugational transfer of pMEARTT results in gook fore which, cones of arowth inhibition that lessing as a ent when a law is every no denor cells develop in a confluent cause to place at a sense receptor. dells. A 6.1-kb pMHA300 IMA region specifying the junctions of conjugation and pook formation was sequenced, revealing 10 open reading frame.s. This it the first sequence of the transfer region of a plasmid from a nonstreptomy sete astinomy sete. No slear similarities were found between the deduced sequences of the 10 putative Tra proteins of pMEA300 and those of Streptomyces plasmids. All Tra proteins of pMEA300 thus may represent unfamiliar types. A detailed mutational anal, showed that at is ast four individual proteins, Traker, 4-- Day, Traker 18,6-6 lay, Trai A .40 to Day, and Inalightally of a , are required for efficient transfer or pMFA: C. Their simpliful resulted in a plear reduction in the conjugational transfer in quencies, rancing from (5.2 times, 101)-fold (Trad) to (2.3) .times. 174 -fold Trad , and in reduced prok sines. At least two you stive yroteins, Trak (17,688 Da) and TraB (31,441 Da), were shown to be desponsible for a post formation specifically. The entropy is a limitable for the

gMEA301-en mided KorA protein to fine traA-alrA intra menin region was obsol 171885-85-1 FI: FRE in perties amino anid sequence; identification and functional anal. of transfer region of plasmid pMEA311 of methylotrophic actin mycete Amy clatopsis mathan liba. => fil req FILE 'REGISTRY' ENTERED AT 13:84:31 ON 13 FEB 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN GUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2.33 American Chemical Society (A'S) Property values tagged with ID are from the DIO VINITI for a file provided by Int. Them. DICTIONARY FILE UPDATES: IL FEB LO + HIGHEST FO 489396-69-1 TSCA INFORMATION NOW CUPRENT THROUGH MAY 20, 2012 Please note that search-term priding does apply when conducting SmartSELECT searches. Crossover limits have been increased. See HELF CROSSOVER for details. Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details: http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf =>= >= > => d .seq 13 1-38- AMSWER 1 OF 38 REGISTRY COPYRIGHT 1003 ADD 487379-77-1 REGISTRY CN GenBank BAA83822 (901) (CA INDEM NAME OTHER NAMES: GenBank BAA83822 (Translated iron: GenBank AB031546) 321 421 201 QEKMKOWNGV TSALFKFFLG TPLKLWASUG HWAIWHFDLW KYTEKQRPRV HITS AT: 232-237 **RELATED SEQUENCES AVAILABLE WITH SEQUINK** LB ANSWER COURTS REGISTRY COPYRISH DITTE AND - 467323-40-0 | FEGISTRY GenBank BAB11133 (901) (CA INDEM NAME) OTHER NAMES: GenBank PAB11233 (Translated iron: GenBank AB016884) 821 258 FI 3301180188 IUROPULOI IWARWEREWU LERUM POEL LUMURTARILO

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CN GenBank CAC42653 (Translated from: JenBank AMIE499),
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    51 KTLMELGMGP LRPWASIGHW LLWHFDLSKY RESEKPRVKI SLAAVFAFMA
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    -4-14-18-48-8 BESINIKE
     Fictein (human clane HFIEC18) (901) (CA INDEM NAME)
OTHER NAMES:
CN 104: PN: US20020165137 SEQID: 104 claimed protein
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F. B. B - 1.2 4
               Aaa-141
uncommon
               A44-145
SQL 175
SEQ 51 AGRIRAGHRA GOTGOWGAWH HOGSWEGSTA SUGETHENTS USGERNHWSA
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REFERENCE 1: 130:340300

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RN 487684-48-9 FE SICTRY
ON - Protein (Mycoba Merium tuberculosis strain (DO1181 dene MT0188) (901) (CA
OTHER NAMES:
   - GerBank AECCG918-derived protein 31 19879104
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OR, I MITHYRERO'S BUARGORIOS MERHEWIDDH BTHADNIEGI ITAGRILLAGO
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**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 137:017411
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   440301-84-8 REGISTRY
CN Protein (Methanosardina madei strain Scel gene MMS191) (901) (CA INDEX
    NAME
MORER MAMES:
CN GenBank AE013459+derived prizein GI U1918753
SQL 276
SEQ 181 LQSRYTFFMA SLIFGILWOL WHEPLIFUKO MYQYRIFHEN IWYAUUPFVG
                            HITS AT: 168-173
REFERENCE 1: 137:74267
L3 ANSWER 9 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 437141-30-5 REGISTRY
CN 6-Phosphogluconolactorase (Arabidopsis thaliana clone RAFL05-08-012
     (R09888) gene At8g24400) (901) (CA INDEX NAME)
OTHER NAMES:
   GenBank AF370305-derived protein GI 13878085
\mathbb{C}N
3QL 219
       -51 GGSLIKSLRK LVESPYUDSI DWARWHFFWV DERUUPKNHD DSNYKLAYDS
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                                 ===::: :
HITS AT: 72-77
REFERENCE 1: 137:28:49
L3 ANSWER 10 OF 38 REGISTRY COPYRIGHT 1003 ACS
   437115-91-8 REGISTRY
CN Protein (human clone US20020048763-SEQID-44744 exon-encoded fragment)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
   4708: FN: US10010048763 SEQID: 44744 blaimed protein
   1 NIIQLLEGET HHGAWQMAWR AWHEKETLME SIEGLR
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**RELATED SEQUENCES AVAILABLE WITH SEQUINK**
REFERENCE 1: 130:04.43
13 ANSWER 11 OF 34 REGISTED MITTER HILL SAN
   - L-Arginine, I-asparaginyl-t-isolog myl-l-isolog myl-l-alut minyl-l-l-alut minyl-l-l-a
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histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-
     tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-
     lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-
     secyl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX
OTHER NAMES:
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CN Protein Chuman blone W001087273-88210-94280 exchences of a shour
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**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 136:351357
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   ANSWER 12 OF 38 REGISTRY COPYRIGHT 2003 ACS
   41:969-90-5 REGISTRY
\mathbb{N}
    L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-
     le cyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-
     histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-
     tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-
     lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-
     seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX
     NAME)
DITHER NAMES:
ON 35: PN: W00157275 SEQID: 33858 claimed protein
IN Protein (human brain clone W00157275-SEQID-33858 exon-encoded fragment)
36 36
    1 NIIQLLEGFI HHGAWQMAWR AWHFKFILME SIEGLE
EQ.
                              == ====
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**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 136:320295
     ANSWER 13 OF 38 REGISTRY COPYRIGHT 2003 ACS
EN 40+874-66-6 REGISTRY
CN Protein (Methanosardina adetivorans strain C2A gene MA1162) (9CI) (CA
     INDEX NAME)
OTHER NAMES:
    Ger.Bank AE010783-derived protein GI 19914997
HQL 28H
    151 LQSRHTFFTA SIFFSILWSL WHFPLIFVNN MYQYEIFHEN VWYAVNFFVS
SEQ
                             ==== = := ::
HITS AT: 168-173
REFERENCE 1: 130:05074
    ANSWER 14 OF 38 REGISTRY COPYRIGHT 2003 ACS
13
    -402671-83-4 REGISTRY
    L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-
    leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-iscleucyl-L-histidyl-L-
    histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-
     tryptophyl-L-arginyl-L-alanyl-1-tryptophyl-L-histidyl-L-phenylalanyl-L-
     lyéyl-l-phenylalanyl-l-isoleusyl-h-leusyl-h-methionyl-h-.alpha.-glutamyl-h-
    seryl-l-15000-4 myl-l-.alpha.-glutamylgly myl-l-ledbyl- (901) - CA INDEX
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 CN 855: PN: W07187270 SEQID: 34889 Flaimed yr rein
221 32
SEÇ 1 NIL, LLEGFI HEGAN, MANE ANHEKFILME GIEGER
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**RELATED SEQUENCES AVAILABLE WITH SEQUINK**
REFERENCE 1: 136:227872
13 ANSWER 16 OF 36 REGISTRY COPYRIGHT 2006 AGS
RM 400957-73-8 REGISTRY
   Protein (human fetal liver blone W00157277-SEQID-33828 ewon-enboded
     fragment) (901) (CA INDEM NAME)
OTHER NAMES:
CN 528: PN: WO0157277 PROID: 33778 Glaimed by Fried
SQL 37
SEQ 1 NIIQLIEGEI HEGAMQMAMR AMBEKETIME SIEGLE
HITS AT: 19-24
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 138:195264
13 AMSWER 16 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 400696-91-5 REGISTRY
  Secretory protein (human clone HNNBM45 53-amino acid precursor) (9CI) (CA
CN
    INDEX NAME:
OTHER NAMES:
CN 96: PN: W00216390 SEQID: 98 claimed protein
NTE
             Aaa-50
Control Control Control Control
SQL 53
   1 MVFLSHLFGT KRLFLLLALI WAGWHFSYMP ADAWUDEGIP DKYLÇAYLSI
SEQ
HITS AT: 21-20
**RELATED SEQUENCES AVAILABLE WITH SEQUINK**
FEFERENCE 1: 130:195341
    AMSWER 17 OF 36 REGISTRY COFYRIGHT 2003 ACS
    400664-75-7 REGISTRY
RN
    L-Arginine, L-asparaginyl-L-isoledcyl-L-isoledcyl-L-glutaminyl-L-ledcyl-L-
    leveyl=L-.alkha.=glutamylglycyl=L-khenylalamyl-L-isolewcyl-L-histldyl-L-
    histidylgiyoyl-L-alanyl-L-tryptophyl-L-gluramonyl-I-m. Thionyl-L-alanyl-I-
    tryptophyl-L-arginyl-L-alanyl-L-ryptophyl-L-histidyl-L-phehylalanyl-L-
    lysyl-l-phenylalanyl-h-isolewcyl-h-lewcyl-h-m-thionyl-h-,alpha.-;hotamyl-h-
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    AMSWER 18 OF 38 FEGISTRY COPYRIGHT 11 8 ACC
    394342-96-2 FEGISTRY
    SPERMIDINE SYMTHASE TRANCMEMERAME PROTEIN OF Wistonia solanwooding strain
     GMI1000 gene speE10 901, CA HMLEM NAME
OTHER NAMED:
    GenBank Alő4e ssá-derived protein 41 1 4:1:1.
SEQ 181 VSLLFPLVLA PRIGIVRIGE LEGIONTAIA VWILWHERAE LGISARIRGA
                                              HITS AT: 182-187
REFERENCE 1: 136:145954
    ANSWER 19 OF 39 REGISTRY COPYRIGHT 2103 ACS
    394342-70-2 REGISTRY
RN
    SPERMIDINE SYNTHASE PROTEIN (Ralstonia solanacearum strain GMI1888 gene
     speE2) (901) (CA INDEM NAME)
OTHER NAMES:
CN GenBank AL646084-derived protein GI 17431779
SQL 525
    151 LVSRVLTFDY LGALAVSLLF PLVLAFRIGE VRTGFLFGLG NTATAVWILW
SEQ
       201 HFFAELGLSA FLEGAMAWFA GMUGAALLAG FAAGUELTHW SERALFGDEI
HITS AT: 197-202
REFERENCE 1: 136:145954
    ANSWER 00 OF 38 REGISTRY COPYRIGHT 2003 ACS
    -354873-95-4 REGISTRY
CN Musculeskeletal-associated antigen (human clone HFIEC13-883185 fragment)
    (9CI) (CA INDEX NAME)
CIHER NAMES:
    1147: PM: W00155367 SEQID: 1158 claimed protein
               F_{2,1,1} = \frac{1}{2} C
              R_{44} = 94
Carrier Car
              A44-1134
               Aan-141
uncommen
                - Ada-140
VEQ - F1 A, B1BA HBA GATH WOLWH F83.WH BRIA CUGHUH BUG UC, FFMEMCA
                           \overline{x} = x^{-1} \cdot x^{-1} \cdot x^{-1} \cdot x^{-1}
HITS AT: 60-71
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M-E-17-7 19_-11.414

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**ABNATED DE, TENDEN ATALDARDE DITE DE, DITER**
 REFERENCE 1: 10x:x8284
          ANSWER 21 OF 38 REGISTRY COPYRIGHT ADDA ACS
          - 369644-15-3 REGISTRY
 on STE: FM: Modiffier objin: 1641 unblaimed protein 901 - DA INDEM MAME
                                            ---- 1 \sim _{\star} tirm ----- _{\star} _{
 SEQ 1 MVFLSHLF3T KRLFLLLALI WASWHFSYMF ADAWUDFGIF DRYLQAYLSI
                                                                                  1 1 1 1 1 1 1 1 1
HITS AT: 21-26
 **RELATED DESCRIPTION AVAILABLE WITH OR LINE: *
REFERENCE 1: 135:335111
          ANSWER 22 OF 38 REGISTRY COPYRIGHT 1013 ACS
L3
          354113-34-1 REGISTRY
           L-Phenylalanine, L-methionyl-L-glutaminyl-L-leusyl-L-prolyl-L-isoleusyl-L-
             tryptophyl-L-leucyl-L-histidyl-L-leucyl-L-seryl-L-seryl-L-tyrosyl-L-
             isoleucyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-tryptophyl-L-histidyl-L-
             phenylalanyl-L-arginyl-L-threenyl-L-methionyl-L-.alpha.-glutamyl-L-leusyl-
             L-isoleudyl-L-seryl-L-alanyl-L-seryl-L-valyl-L-leudyl-L-seryl-L-valyl-L-
             .alpha.-aspartyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-leucyl-L-
             leucyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
             176: PN: WO0157187 SEQID: 176 claimed protein
             Bone marrow-specific protein (human clone WO0157187-SEQID-176 precursor)
SUL
           .13
                       1 MOLFIWLELS SYIWLIWEER IMELISASUL SUDLLILGLE YKE
SEQ
                                                                 ======
HITS AT: 14-19
REFERENCE 1: 135:163431
          ANSWER 13 OF ART REPLATED IN FYRIGHT 1 FROM
          353308-77-3 REGISTAY
         Bone marrow-specific protein Chuman Flone WDolf Tem-SE, 12-364
             contid-encoded precursor (901) (0A INDEM NAME
OTHER NAMES:
          361: PN: WOO157187 SEQID: 364 blaimed protein
                                        ----- logation ----- description
SQL 96
SEQ 51 FWHMQLFIWL HLSSYIWLIW HFRIMELISA CULSUPLIEL GLIFKE
                                                                      HITS AT: 67-71
REFERENCE 1: 181:188:38
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1111111

MoHelbey 10 41.414

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ANSWER NA OF the REGISTRY COSPYRIGHT 2008 ACC
    andu George REGITTRY
 du - Protein human blome HFIEDla 1901 - DA INDEM NAME
 CTREE NAMES:
 ON 94: PM: WOOLESAAM SEQIM: 174 blaime: protein
                 ----- logation ----- description
un dommor. Aga-36
                 _____
                in 1 4 = 1 . . 4
 \mathcal{Z}_{2}:=\left\{\begin{array}{ll} 1 & 1 \\ 1 & 1\end{array}\right\}
 n n Min i te i ni evi evi i te i vi
nak k k na na na karakara tan k a
                 = A_{i+1} + A_{i+1}
SEQ 51 AQRIRAGHRA GGTGCWGAWH FSGSWRGSLA SVGPVPPNVS VSQPFXFXSA
HITS AT: 66-71
 **PELATED OBJUENCES AVAIDABLE WITH SETTINE**
REFERENCE 1: 135:163414
L3 ANSWER 25 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 343286-49-7 REGISTRY
CN Protein LMRP (Physcomitrella patens clone 55 ck5 b04fwd lipid
     metabolism-related) (9CI) (CA INDEM NAME)
OTHER NAMES:
ON 241: PN: W00135141 SEQII: 156 31 (156) 8 135611.
SQL 173
SEQ
    51 PATKTLMENG MGPLRPWASI GHWLLWHFDI SKYRESEKPR VKISLAAVFA
HITS AT: 73-78
REFERENCE 1: 135:19831
L3 ANSWER 26 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 307998-10-3 REGISTRY
     Desaturase, fatty acid .cmega.6-(Chlamydomonas strain W-80) (9CI) (CA
     INDER NAME!
801 421
    201 QEKMKDWNGV TSALFKFFIG TELKLWASVG HWAIWHEDLN KYTEKQRPRV
SEQ
HITS AT: 232-237
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 134:2473
L3 ANSWER 27 OF 39 REGISTRY COPYRIGHT 1113 And
   302645-66-5 BESTSTRY
     Protein Arabii pala thaliana tha na taka 11.111 at the Arabii Arabii
CN 969: FN: EF103-408 SEQID: 1 - 164 Million protect.
8$1 256
SE. - 81 GROLIKOLBK LUESEYULDI LWARWHEEWU DERUUEKUHO DENYKLAYOS
HITTO AT: "1-"T
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RELATED SEQUENCES AVAILABLE WITH SEQUINK

REFERENCE 1: 133:318297

L3 ANSWER 28 OF 38 REGISTRY COFYRIGHT 2003 ACS

RN 302645-65-4 REGISTRY

ON Protein Arabidopsis thaltana olune Ceres [21421477 FOT CA THUEW NAME

OTHER NAMES:

UN 968: PN: EF1033408 SEQID: 60968 claimed protein

HQL 325

BEQ 101 ADISDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD

MITS AT: 141-146

REFERENCE 1: 133:318297

13 ANSWER 29 OF 38 REGISTRY COPYRIGHT 2003 ACS

EM 302411-43-4 REGISTRY

UN Protein (Arabidopsis thaliana clone Ceres_2113368) (901) (CA INDEX NAME)

DTHER NAMES:

MN 163: PN: EP1033405 SEQID: 55163 claimed protein

FQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWU DERVVPKNHD DSNYKLAYDS

======

HITS AT: 72-77

F.EFEF.ENCE 1: 133:318296

L3 ANSWER 30 OF 38 REGISTRY COPYRIGHT 2003 ACS

F.N 302411-42-3 REGISTRY

Protein (Arabidopsis thaliana clone Ceres 2113367) (9CI) (CA INDEX NAME)

DTHEF NAMES:

N 162: PN: EP1033405 SEQID: 55162 claimed protein

EQL 325

JEO 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD

=====

HITS AT: 141-146

FEFERCE 1: 133:318296

13 AMSWER 31 OF 38 REGISTRY COPYRIGHT 2003 ACS

FN: 301564-27-2 REGISTRY

CN Protein (Arabidopsis thaliana clone Ceres 1025180) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1596: PN: EP1033405 SEQID: 7409 claimed protein

30L 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS

=====

HITS AT: 72-77

REFERENCE 1: 133:306360

13 ANSWER 32 OF 38 REGISTRY COFYRIGHT 2003 ACS

RN 301564-06-1 REGISTRY

NTHER NAMES:

VN 1895: PN: EP1/334/8 SEQID: 7408 SlaimAd Erstein

SQL 328

Miffelbey (19,912414

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SE, 111 ADDA ME ME BOARTOODA GOLIFODAMI VESPYODIO WARWHEEWO
HITS AT: 141-148
**RELATED SEQUENCES AVAILABLE WITH SEQUINK**
REFERENCE 1: 133:306361
   AMSWER 33 OF 33 PERIOTRY CORPERTMENT 1913 And
    CN L-Phenylalanine, L-tryptigmyl-L-valy.-L-alany.-L-tryptigmy.-l-m.stray.-
     (901) (M) INDER NAME
OTHER NAMES:
CM 13: PM: Wolldaall1 SEgib: Wallandlaimed Reducence
SQL 6
SEQ 1 WURWHE
1111 HT: 1-6
REFERENCE 1: 133:145915
L3 ANSWER 34 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 286839-22-3 REGISTRY
    L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl-
     (901) <sup>1</sup> (OA INDEX MAME
CN 12: PN: W00044771 SEQID: 21 unclaimed sequence
SOL 6
SEQ 1 WARWHF
          ==:": =: =: =
HITS AT: 1-8
REFERENCE 1: 193:148918
1.3
   ANSWER 35 OF 38 REGISTRY COPYRIGHT 2003 ACS
    286839-16-5 REGISTRY
RN
    L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl-
     (901) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: W00044771 SEQID: 2 claimed sequence
SOL 6
   1 WIRNEE
          HITS AT: 1-6
REFERENCE 1: 133:145915
L3 ANSWER 36 OF 38 REGISTRY COPYRIGHT 0003 ACS
RN 208786+02-1 REGISTRY
    -Brotein Bullian Mysobisterlum tubers, busers busers by the French A. DUBER
    NAME
OTHER NAMES:
   GenBank ADID1418-derived protein 31 (+1;016
SQL 230
   1 MITRYKERSS FVARSOGIOR KREHIWIUWH ETRADULEGI ITAGRILADO
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Fage 45

HITT ALL $1 \times - \cdot 1$

RELATED SE, VENDES AVAILABLE WITH SE, LINK

REFERENCE 1: 130:120305

FEFFERNCE : 1. : The second

13 ANOMER 37 F 34 REGISTRY MORRISHT USES AND

8N 2042D8-11- REGISTRY

CN Desaturase, fatty acid .cmega.6- [Chlamydomonas reinhardtii clone pCDI gene des6 reduced] (GCI) (CA IMDEM NAME)

OTHER NAMES:

CU .omega.6 Desaturase Chlamydomonas reinhardtii blune pCDI yene des6 reduced

TW SenBank Ab. Ted -derive a protein 31 dekemin

SQL 424

SEQ 201 VTEADMAKWD STSAMLYKVF LGTPLKLWAS VGHWLVWHFD LNKYTPKQRT

HITS AT: 234-239

REFERENCE 1: 128:21493"

L3 ANSWER 38 OF 38 REGISTRY COPYRIGHT ALLS ADD

RN 171885-85-1 REGISTRY

CN Protein TraH (plasmid pMEA3001 [901] DA INDEM NAME

OTHER NAMES:

CN Protein TraH (Amydolatopsis methanolida plasmid pMEA300)

SQL 115

SEQ 1 MFTPEFKPTT DHTGQSTTEA VEARRAADLA IYTNAKYPTR TTQTVSWIGW

51 HFGELSGVVV PLGLGAAVWD GFYALSLLTA LGWAANELRL RRQQRAVRTR

==

HITS AT: 47-52

REFERENCE 1: 124:47157

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=> fil hearlus
FILE 'HOAFL'O' ENTERED AT 18:57:58 ON 13 FEB 2003
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FILE COVERS 1907 + 18 Feb 2003 | WOL 188 188 7
FILE LAST MEDATED: 12 Feb 2008 (20081212 ED
 This file contains CAS Registry Numbers for easy and accurate
 substance identification.
=: •
=:.
=> d stat gue 115
              1 SEA FILE=REGISTRY ABB=ON PLU=ON WVRWHF/SQSP
          1110 SEA FILE=REGISTRY ABB=ON PLU=ON W[GAILVSTKRHF] [GAILVSTKRHF]W[
                GAILVSTKRHF]F/SQSP
            -38 SEA FILE=REGISTRY ABB=ON FLU=ON W[JAILUSTR][GAILUSTR]WHF/DQGR
             1 SEA FILE=HOAPLUS ABB=ON PLU=ON L1
            27 SEA FILE=HCAPLUS ABB=01 Filt (11 11)
             1 SEA FILE-HOAPLUS ABB-ON PLU-ON 18 AND 16
             TP SEA FILE-REGISTRY ABBRON FIND-ON L2 AND SQL-<50
             58 SEA FILE-HCAPLUS ABB-ON FLU-ON 1112
             18 SEA FILE=HCAPLUS ABB=ON FLU-ON L18 MOT (2003 OR 2002)/FY 17 SEA FILE=HCAPLUS ABB=ON PLU=ON L14 NOT (16 OR LT)
L15
== `.
=> d ibib abs hittm 118 1-17
L15 ANSWER 1 OF 17 HCAFLUS COPYRIGHT 2003 ACS
                          2002:36295 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                          Musleis asids and their enseted polypoptides in mo
                          human tissues
INVENTOR(S):
                          Tang, Y. Tom; Liu, Thenghra; Drmanac, Radoje T.
PATENT ASSIGNEE (3):
                         Hysed, Inc., USA
                          FOT Int. Appl., 141 pp.
                          C.CEN: FIRMS
DOCUMENT TYPE:
                          Patent
LANGUAGE:
                          PATENT INFORMATI M:
```

PATENT NO. MIND DATE APPLICATION NO. DATE

```
W: AB, AB, AL, AM, AT, AM, AA, BB, BB, BB, BT, BB, BA, BB, BT,
            CH, CU, CE, CH, CH, CU, CC, EE, ES, EI, FF, GI, FE, FE, FF, EF,
            HT, ID, IL, IN, IS, IP, HE, HG, HE, HE, HU, LY, LH, LS, LY, LT,
            Y', ZA, CE, AM, AD, BY, KY, KY, KY, KY, CY, CY, CX, CX, AT, BE, CY,
            IE, DE, ES, EI, ER, GB, NR, IE, II, LM, MN, NL, ET, CE, TS, BF,
    BJ, CF, CG, MI, CM, GA, MI, GM, MI, MR, MR, CM, TD, TE
AU 2001038347 AS 200103012 AT 2001-38647 2001 22,
                                     i ka zina-isaka in inti wwa
                                    US 2000-815126 A 20000225
                                      US 2000-577409 A 20000518
   The present invention provides a collection or library of 13,901 nucleic
\Xi\Xi
    acid contig sequences assembled from empressed sequence tag or cDNA
    libraries isolated mainly by sequencing by hybridization (SBH), std. PCR,
    Sanger sequencing techniques, and in some cases, sequences obtained from
    one or more public databases. The office libraries are from human tissue
    sources and nearest neighbor sequence homologies are provided. The
    invention also relates to the proteins encoded by such polynuclectides,
    along with therapeutic, diagnostic and research utilities for these
    polynucleotides and proteins. [This abstr. record is the fourth of four
    records for this document necessitated by the large no. of index entries
    required to fully index the document and publication system constraints. [.
ΙT
    432700-32-8
    RL: ANT (Analyte); BSU (Biological Study, unclassified); PRE Executive;
    THU (Therapeutic use ; AND) Analorical and by ;
    USES (Uses)
       (amino acid sequence; nucleic acids and their encoded polypeptides from
       human tissues!
L15 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:898070 HCAPLUS
DOCUMENT NUMBER:
                     137:16519
                      Human polypeptide fragments and their encoding cDNA
TITLE:
                       golymuslettidos
                       Shimkets, Richard A.; Leach, Martin D.
PATENT ASSIGNEE(S):
                       Curagen Corporation, USA
                       FCT Int. Appl., 1037 pp.
SOURCE:
                       CODEN: FIXXD2
DOCUMENT TYPE:
                       Patent
LANGUAGE:
                       English
FAMILY ACC. NUM. SOUNT:
PATENT INFORMATION:
    PATENT NO.
                                        A2
    WO 2001092523
                                        WO 2001-XA10836
                                                       20010529
        W: AE, AG, AL, AM, AT, AU, AC, EA, BB, BG, BR, BY, BZ, CA,
                   CT, CD, DE, DK, DM, DD, EE, ES, FI, GP, GD, GE,
            HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KE, MD, RU,
        BW: GH, GM, KE, LS, MW, MD, SD, SL, SD, TD, TG, DW, AT, BE,
                                          FS, MI, FB, 4B, 46, IM,
                   OG, OI, ON, OA, ON, OW, NI, MR, NE, SN, TD,
        W: AE, AG, AL, AM, AT, AU, AD, BA, BB, BG, BR, BY, BD, CA,
            CO, CR, CO, CU, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE,
            HR, HU, ID, IL, IN, IS, JF, KE, KG, KF, KR, KZ, LC, LK, LR, LS,
            II, II, IX, MA, MD, MG, MK, MM, MK, MM, MI, MG, MI, EI, EI, ET, EO,
```

FX: 38, 32, 8F, 77, 28, 27, 21, 21, 22, 77, 78, 78, 81, 88, 78,

RU, SI, SE, SR, SI, SK, SL, TJ, TM, TB, TT,

YN, YN, CA, CE, AM, AZ, BY, KR, KZ, MD, BY, TI, TM

DE, DK, ES, F1, FF, GB, FR, IE, IT, LV, MY, ML, FT, SE, TF, BF, EV, CF, CG, C1, CM, FA, EM, GW, ML, MR, ME, SM, TD, TG

PRINTITY APPLN. INFO::

US 2000-208132P P 20000030
US 2001-208132P P 20000030
US 2001-208132P P 20000030
W. 2001-4080099, W 20010029

The present invention provides 11,491 GRFM, novel human polypeptide fragments, as well as the 11,491 gDNA fragments endoding GRFM and antibodies that immunospecifically bind to GRFM or any derivs., variants, mutants, or fragments of the GRFM polypeptides, polynupleotides, or antibodies. The invention addnl. provides methods in which the GRFM polypeptides, polynupleotides, and antibodies are used in detection and treatment of a broad range of pathol. States, as well as to their uses. [This abstr. resord is one of time reserving to the constraints and publication system constraints.].

IT 434378-63-9P

CORPORATE SOURCE:

RL: ANT (Analyte); BFN (Biosynthetic preparation); BSU (Biological study, unclassified); FRP (Properties); THU (Therapeutic use); AMST (Analytical study); BIOL (Biological study); FREP (Preparation); USES (Uses) (amino acid sequence; human polypertide tragments and their encoding cDNA polynucleotides)

L15 ANSWER 3 OF 17 HCAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:273192 HCAPLUS

DOCUMENT NUMBER: 133:295042

TITLE: Selection of an immunogenic and protective epitope of

the PsaA protein of Streptococcus pneumoniae using a

phage display library

AUTHOR(S): Srivastava, N.; Zeiler, J. L.; Smithson, S. L.;

Carlone, G. M.; Ades, E. W.; Sampson, J. S.; Johnson,

S. E.; Kieber-Emmons, T.; Westerink, M. A. J. Department of Medicine, Medical College of Ohio,

Toledo, OH, 43614, USA

SOURCE: Hybridema (2000), 19(1), 23-31

CODEN: HYBRDY; ISSN: 0272-457M

PUBLISHER: Mary Ann Liebert, Ind.

DOCUMENT TYPE: Cournal LANGUAGE: English

AB Streptocopous theunoniae is an intertain that describes itsease in young and elderly individuals. The currently available polysaccharide vaccines have limited efficacy in those age groups most susceptible to pneumococcal infections. This study focuses on mapping the epitopes of a surface protein of S. pneumoniae by biopanning a 15 mer phage display library using 5 different monoclonal antibodies (MAbs) against the Pheumoccal surface adhesin A (PsaA). PsaA is a component of the bacterial dell wall that is highly species specific and is involved in bacterial adherence and virulence. Biopanning of the phage display library reveals three distinct epitopes on the PsaA protein. The sequence homol. of these epitopes ranges from two to six amino acids when compared to the native FsaA protein type 2. Two of these epitopes have been evaluated for their immunogenicity in mice. The peptide selected by the MAbs 8G12, 6F6, and 187 is referred to as the consensus pertide and is immunogenic in mice. Optimal anti-PsaA response is obsd. in mice immunized with 50 .mu.s of the consensus peptide complexed to proteosomes in 1:1 ratio. The anti-PsaA response is significantly I were than the response to the lead native protein. The pertibute leave beyon not have here by a continue of the pertect of the factor form is similifyingly protection for a communication of which is an arranged serotype in when compared to mise irrunded with the native protein. These results show that the selector opings of law protein are immunipalit and protestive in mise. These equitopes need to be evaluated further as alternatives to currently available bassines.

301300-56-1

Moderntey 109 Models FL: FAC Figligal activity or effector, except aiverse ; FAU Fibligibal study, unclassified ; THY Therapeutic use ; BICL Bitlogical study ; USES (Uses) "PsaA protein of Streptodovous pheum niae in vaddine against strepto doppal infections REFERENCE COUNT: 64 THERE ARE 64 MITEL PREFERENCE. AUXILIABLE E E 1811 BETBILDING TOTALL OUT AVAILANCE LINE FROM FRANCE 1115 ANSWER 4 OF 17 HOAFINS TOFFFICHIOLOGY AND ACCESSION NUMBER: 1894: NOT LUN HOMPION 131:198616 Epitope peptides immunogenio against Streptobodous y neumoniae and their use in vaccines INVENTOR(S): Carlone, George M.; Ades, Edwin W.; Sampson, Jacquelyn S.; Tharpe, Jean A.; Zeiler, Joan Louise; Westerink, - Maria Anna Julia FATENT ASSIGNEE D.: The Dovernment of the United States of America, kepresented by the Secretary, USA SOURCE: FOT Int. Appl., 59 pp. CODEN: PIKKD2 Fatent LANGUAGE: English FAMILY ACC. NUM. COUNT: 1 PATENT INFORMATION: PATENT NO. KIND DATE WO 9945121 A1 19990910 WO 1999-US4626 19990226

MO 9945121 A1 19990910 W0 1999-US45A6 19990226

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, 3M, HR, HU, ID, II, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MN, NO, NZ, FL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TU, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AD, BY, KG, KZ, MD, RU, TJ, TM

EW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, UW, AT, BE, CH, CY, DE, DK, ES, FI, ER, UB, UB, IE, IT, LU, MC, ML, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2326408 A1 19990910 A0 1999-2326408 19990226

BR 9908476 A 20001205 BR 1999-8476 19990226

EF 1060249 A1 20001200 EF 1999-908543 19990226

ER: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRIORITY AFFLM. INFO.:

US 1998-70868F F 1998/302

WO 1999-US4326 W 19990226

AB Peptides are provided which immunospecifically bind to monoclonal antibodies specific for the ST-kDs pneumocopus surface adhesion A provein (PsaA) of Streptocopus pneumoniae of the invention, and that are immunogenic against Streptocopus pneumoniae inferritm. Also provided are vaccines comprising such immunogenic polypeptides, and methods of conferring protective immunity against Croeptocopus pneumoniae inferrites of the invention. Also provided are methods of detecting the presence of Streptocopus pneumoniae in a sample using antibodies or antigens, and methods of preventing and treating Streptocopus pneumoniae infection in a subject. In addin, a phage display method of identifying the sequence of a poptide potentially expable of eliciting protective immunity against a pathogenic microcryanism is provided.

TT 241814-51-7P

BL: BIN Bi synthetic preparation; FRE Properties; THU Therapeutic use; bloc Biological study; FREE Freeparation; USES Uses: (epitope peptides immunogenic adainst Streptococcus pneumoniae and their use in vaccines.)

20 956 1 they () + (41.414)

REFERENCE COUNT: 5 THERE ARE & CITEU REFERENCES AVAILABLE FOR THIS FROMES. ALL STRATESMS AVAILABLE IN THE BE FORMAT

115 AMSWER 5 OF 1" HOAFLUS COFFEIGHT 1005 ACS

ACCESSION NUMBER: 1998:488041 HOAPING

DOCUMENT NUMBER: 129:78489

TITLE: Heparin- and sulfatide-binding peptides from the type

I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other

thereof for treatment of metastatic tumors and

necvascularization-related diseases

INVENTOR'S:

Roberts, Tavid D.; Browning, Philip J.; Bryant, Joseph L.; Inman, John M.; Heutesch, Henry C.; Bul, Neighua

FATENT ASSIGNEE(S): United States Dept. of Health and Human Jervices, USA

SOURCE: U.S., 183 pp., Cont.-in-part of U.S. 215,0%5,

abandoned.

CODEN: TOWARK

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5770563 US 801812		19980623 19921215		19950607 19911206
US 5357041 US 6051549	$rac{\mathcal{A}}{A}$	19941018 20000418	US 1998-41119	19980311
PRIORITY APPLN. I	INFO.:		US 1994-215085 B2	19911206 19940321 19950607

OTHER SOURCE(S): MARFAT 129:76489

AB This invention identifies a biol. active group of peptide sequences from Type I repeat units of the extracellular matrix protein, human thrombospondin-1, identical or homologous to the sequence, KRFKQDGGWSHWSPWSSC (SEQ ID NO:30). The biol. activities residing with the full sequences, portions thereof, and variants of the full or a similar sequences are disclosed. The invento is assorbed to be a control of apbe enhanced by covalently linking these postudes to a litural contains, preferably a branched, water-sol. polymer or low or absent) to misity and immunogenicity, such as polysucrose (Fiscall). The invention describes (1) a method for prepg. such conjugates, (2) the use of the defined peptides or their conjugates in blocking or modifying the action on cellular processes of heparin (e.g., proliferation, adhesion, motility, extravasation and neovaspularization', sulfatides, related sulfated glycoconjugates, fibrenectin, and basic ribroblast growth factor, involving malignant cell lines and normal endothelial cells. The defined peptides, analogs or peptidomimetics and their conjugates for treatment of metastatic tumors, breast carcinomas, melanomas, Kaposi's sarcomas, hemangiomas, diabetic retinopathies, and various pathol. conditions dependent upon neovascularization is also disclosed.

IT 209457-55-6

RL: BAC (Biological activity or effector, except adverse); BFR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses) (heparin- and sulfative-binding pertides from the type I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other nectascularination-related diseases

tumors and other nectasoniaridation-related diseases:

REFERENCE COUNT:

28 THESE ARE 1- CITED REFERENCE IN THE RESEARCH MADE AND THE RESEARCH FOR THE RESEARCH

115 ANSWER & OF 17 HUAFIUS COMMSIDET 1 18 AND ADDESSION NUMBER: 1899:0, 4083 HEAFIUS 1007UMENT NUMBER: 1007:4184

M Melvey 13 812414

A region from the medium chain adaptor subunit (.mu.) recognices leucine- and tyrosine-based sorting signals AUTHOR (3): Eremnes, Tobil; Lauvrak, Vigdis; Lindqvist, Bjorn; Bakke, Lidmuri Dep. Molecular Call Bl 1., little on Bl 1 my, Unit. COMPURATE SIMPOR: ourse, followersky to rusy Sturnal or Biological Themletry (1949), we told , SOUTHOE: ÷, -- ÷, ; CONEM: CHOHAS; ISSN: 0 21-9204 American Society for Bilchemistry and Molecular PUBLISHED: Journal En ilish AB Tyrosine-based surting signals in the sytosolic tails of membrane proteins have been found to bind directly to the medium chain subunit (.mu.) of the adaptor complemes AF-1 and AF-2. For the leucine-based signals, an interaction with AF-1 and AF-2 has been reported, but no specific interacting subunit has been demonstrated. After searching for mols. interacting with the leucine-based sorting signals within the cytosolic tail of the major histocompatibility complex class II-assocd. invariant chain using a phage display approach, we identified phage clones with homol, to a conserved region of the AF-1 and AP-2 .mu. chains. To investigate the relevance of these findings, we have expressed regions of mouse .mu.1 and .mu.2 chains on phage gene product III and investigated the binding to tail sequences from various transmembrane proteins with known endosomal targeting signals. Enzyme-linked immunosorbent binding assays showed that these phages specifically recognized peptides contg. functional leudine- and tyrosine-based sorting signals, suggesting that these regions of the .mu.l and .mu.2 chains interact with both types of sorting signals. 208192-30-7P RL: BPN (Biosynthetic preparation,; BIR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); FREP (Freparation); PROC (Frocess) (region from medium chain adaptor subunit (.mu.) of AP-1 and AP-2 recognizes leucine- and tyrosine-based sorting signals) REFERENCE COUNT: THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS 44 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT LIS ANSWER 7 OF 17 HOAFLUS COPYRIGHT 2013 ACS ACCESSION NUMBER: 1998:11596 HCAPLUS 128:110913 DOCUMENT NUMBER: Amino acids within residues 181-200 of the nicotinic TITLE: acetylcholine receptor .alpha.1 subunit involved in nicotine binding ACTHOR(S): Lentz, Thomas L.; Chaturvedi, Vijaya; Conti-Fine, CORPORATE SOURCE: Department of Cell Biol by, Yale University John 1 of Medition, New Haran, M., from = , 1998. Bischemical than and say (1998), if σ , satisfied SOURCE: COTEN: BOYCOR: ISON: IT RELEADED Elsevier Science Inc. FUBLISHER: DOCUMENT TYPE: Journal LANGUAGE: Er. Tlish Structural determinants of L-[3H] nicotine binding to the sequence flanking Cys 190 and Cys 198 of the Torpedo agetylpholine receptor .: slphq.1 subunit were investigated using synthetic peptides residues [81-000] and fusion proteins residues 100-11 . Misstine binding at a single con m. (so nM) was compared with 'I paytides and fusion proteins in which individual amin. a dide at gusitions 181-200 were substituted. Substitution of Lys 1:5, Tyr 195, Tys 191, Tys 193, Thr 196, and Tyr 198 resulted in the dreatest redn. in his time binding. Equil. binding of [3H] hisotime to populds [51-0]) revealed a binding component with an apparent KD of 1.2

.ma.M. Daletitation i bye let with hat, His 1et, lyr 1et, Tye 1et, Tye 193, and Tyr 198 resulted in a significant redn. in affinity. Affinity was not affected significantly by substitution of Arg 182, Tys 185 (with Gly or Arg., Val 188, Tyr 189, Pro 184, Asp 185, Thr 198, and Asp 200. It is concluded that Lys 1-8, His 1+8, Tyr 190, Dys 190, Cys 190, and Tyr 198 play the greatest role in microtine binding to residues 191-200 of the laikha.1 supunit. Freditus studies have implitated Tyr 19, 19s 191, 19s Iva, and Iva Iva in aganist binding to the abstyloholine receptor. These results of milimum and he con these residues and also demonstrate a function for Lys 1-1 and His 160 in nigotine binding.

201529-09-1

RL: BPR (Biological probess); ESU (Biological study, unclassified); PRP 'Properties'; BIOL 'Biblogical study); PROC 'Process' (181-200 midetimie reseptor .alpha.1-subunit mutant; midetimie adetylcholine receptor lalpha.1 subunit residues 191-2/1 in hisotine binding;

LIS ANSWER 8 OF 17 HOARDOO DORYNIGHT OF ACCESSION NUMBER: 1990:83391 HMARDOS

DOCUMENT NUMBER: 124:114958

Isolation and characterization of antibodies which

specifically recognize the peptide encoded by exon 7

(v2) of the human CD44 gene

Borgya, A; Woodman, A; Sugiyama, M; Donie, F; AUTHOR(S):

Kopetcki, E.; Matsumura, Y; Tarin, D

CORPORATE SOURCE: Poshringer Mannheim GmbH, Fondberg, D-81871, Germany SOURCE: -Clinical Molecular Pathology (1995), 48(5), M241-M250

CODEN: CMPART; ISSN: 1355-2910

PUBLISHER: BMJ Publishing Group

DOCUMENT TYPE: Journal English LANGUAGE:

AB Exon 7 of the human CD44 gene is overexpressed in many commonly occurring carcinomas. The aim of the study was to explore the diagnostic and therapeutic potential of this frequent abnormality. A new monoclonal antibody (mAb, M-23.6.1) and a polyslonal antibody (pAb, S-611" to the corresponding antigen were raised by immuniting mide and shoep, resp., with a specially constructed fusion protein HIV2 (qp32)-CD44 exon 7. Characterization of mAb M-23.6.1 by ELISA, Western blotting, immunocytochem., and FACS anal. confirmed that it specifically recognizes an epitope in the region between amino acids 19 and 33 of the reptide encoded by this exon. Western blotting expts. with two sell lines, RT111 and ZR75-1, known from RT-FCR data to be over-transcribing the exon, yielded a monospecific band of approx. ALC kDa, and immunocytochem. showed discrete membrane staining on the same cell lines. Fluorescent antibody cell sorting (FACS) revealed binding to greater than 90% of the cells of each of these lines. Specificity of recognition of the antigen was shown by inhibition of the precise immunoreactivity typically seen in ELISA and Western blots, by pre-incubation with synthetic exon 7 peptide or fragments of it. The new antibodies will be useful tools for the further anal. of abnormal CD44 isoforms and their clin. implications.

172997-35-2

RL: BFR (Biological process'; BSU (Biological study, unclassified); BIOL (Biological study); PRAC (Process) (isolation and characterization of monoplonal antibody to poptide encoded by exon 7 of human CD44)

115 ANSWER 9 OF 17 HOAPLUS COPYRIGHT 1113 ACS 1995:930102 HOAFING ACCESSION NUMBER:

DOCUMENT NUMBER: 113:330019

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                         leg. Chemical Immunology, Weinmann Inst. Solence,
CORPORATE SOURCE:
                         Religion, TVIII, Istael
                         Proceedings of the Mational Academy of Ociences of the
2377321:
                         United States of America (1990), 92 23 , 178 1-8
                         CODEN: PNASA6; ISSN: 0027-8424
                         Mati hal Anademy i Onlehnes
                         English
AB The ligand binding site of the mistinis as tylocoline reset of Arth B
     is localized in the lalkha. - Subunit within a a nach that a the tanker
     OyselkL and elm. By analyzing the single itemsed in it Arm B is a
     animal species that are resistant to lalknal-neurotowins, the authors have
     previously shown that for residues in this region, at positions 167, 189,
     194, and 197, differ between animals sensitive (e.g., mouse) and resistant
     (e.d., manuages and snake) to lalpha.-bungaratowin (lalpha.-BTW). In the
     present study, the authors performed site-directed mutagenesis on a
     fragment of the mongoose AcChoR .alpha.-subunit (residues 122-205) and
     exchanged residues 187, 189, 194, and 197, either alone or in combination,
     with those present in the mouse .alpha.-subunit sequence. Only the
    mendeese fragment in which all four residues were mutated to the mouse
     ones exhibited .alpha.-BTX binding similar to that of the mouse fragment.
    The mongoose double mutation in which Leu-194 and His-197 were replaced
    with proline residues, which are present at these positions in the mouse
    AcchoR and in all other toxin binders, bound .alpha.-BTX to .apprxeq.60%
     of the level of binding exhibited by the mouse fragment. In addn.,
     replacement of either Pro-194 or -197 in the mouse fragment with serine
     and histidine, resp., markedly decreased .alpha.-PTM kinding. A. Lorher
    mutations resulted in no or just a small introder on laying. - HIM sinking.
     These results have led the authors' to propose two subsites in the kinding
    domain for .alpha.-BTX: the proline subsite, which includes Pro-194 and
     -197 and is crit. for .alpha.-BTX binding, and the arcm. subsite, which
    includes amino acid residues 187 and 189 and dets. the extent of
    .alpha.-BTX binding.
    170662-94-9, EARGWKHWNFYACCLITHYLD 170662-98-3,
    EARGWKHWVFYACCFTTHYLD 170662-99-4, EARGWKHWVFYACCLTTFYLD
    170663-00-0, EARGWRHWVFYACCPTTPYLD
    RL: BFR (Biblogical process); ESU (Biblogical study, unclassified); FRF
     (Froperties); BIOL (Biological study); PROC (Process)
        (mongoose nicetinic receptor .alpha.-subunit binding domain mutant
       dentg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding
        domain arom. subsite and proline subsite)
    170663-01-1, EARGWKHWVFYSCOPTTPYLD
     RL: BFR (Biological process); BSU (Biological study, unclassified); FRP
     (Properties); BIOL (Biological study); FROC (Frocess)
        (mouse nidotinio receptor .alpha.-subunit kinding domain conta.;
       nicotinio receptor .alpha.-subunit .alpha.-bungaror win-sinding dimain
       arom. subsite and proline subsite'
    170663-02-2, EARGWKHWVFYSCWPTTPYLD 170663-03-3,
     EARGWKHWVFYSCOSTTPYLD 170663-04-4, EARGWKHWVFYSCOFTTHYLD
    RL: BFR (Biological process); BSU (Biological study, unclassified); FRF
     (Proportios); HIOL (Biological study ; 1800 Fromes
        (mouse nicotinic receptor .alpha. -submit binding domain mutant contg.;
       nisotinis resentor .alpha.-subunit .alpha.-bun marstokin-binding domain
       arum. Subsite and proline subsite
LIS AMSWER 10 OF 17 HOAPLUS COFYRIGHT 2003 ACS
ADDESCION NUMBER:
                         1884:018184 HOAFINS
DOCUMENT NUMBER:
                         121:233399
                        Profile of the regions of abetyloholine receptor
                         laight. Sittin recognized by T-lymphocytes and by
                        antibodies in EAMS-susceptible and non-susceptible
                        mouse strains after different periods of immunication
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AUTHOR S,:
                        Oshima, Minami; Fashner, Andrew R.; Atasel, M. Couhair
                        Dep. Biochem., Baylor Coll. Med., Houston, TM, 77031,
CORFORATE SOURCE:
                        Male malar Imm. 0.515 py 13 44 , 35 11 , 433-43
STEEDE:
                        Dulen: M 10174; 1220: 1.1- 23
                        il Attal
                        Er. mish
AB 08781/6 (B6) mice develop a neuromuscular disease, emptl. autoimmune
    myasthenia gravis (EAMG), after .gtoreq.2 immunizations with Torpedo
    dalifornida abetylicholime redeptor (AChR). To det. whether EAMG is
    related to recognition of particular region(s) on the main extracellular
    domain of the .alpha. chain (residues .alpha. 1-210) in prolonged
    immunication, the authors have examd. the differences in the antibody and
     Theeline of this intimetric profiles of Berand CVI and extrain that does not develop
     EAMG) mice after different periods and a no. of immunication with Torpedo
    AChR. In a given strain, antibodies and T cells recognized immunoduminant
    regions, which may coincide or may be uniquely B cell or T cell
    determinants. Both B6 and SJL exhibited Similar antibody recognition
    profiles after the 2nd and through the 4th irruning tions with ACAP. Mail r
    differences between the 2 strains were i and in their Totall recondition
    of regions in the second part (residues 1.1-01), or the main extra mellular
    domain of the .alpha. chain. I delis of SJL recognized ministently only
     one region (111-126) within this part of the Lalpha. Chair, whereas in B6,
     T cell recognition of 3 peptides (111-126, 146-162, and 182-198) and next
    neighbor regions to them persisted throughout the period. Of these 3
    peptides, 146-162 was an immunodominant peptide unique to B6, as the other
     2 peptides (111-126 and 182-198) were also recognized by either T cells or
    antibodies in SJL. To study the role of T cells recognizing region
     146-162 in EAMG, a T cell line was generated against this region and the
     dells transferred into B6 mide followed by one Torpedo AChR injection.
     Enhancement of antibody prodn. toward .alpha. chain peptides was obsd. as
     an influence of T cell transfer compared to profiles at 1 wk. In addn., 1
     out of 3 mice examd. showed signs of EAMG. These results suggest the
    importance of T cells recognizing residues 146-152 in EAMG. Thus, the
    presence of persistent T cell responses to the second half (residues
    100-210) of the main extracellular domain of the .alpha. chain is assocd.
    with the development of EAMG in B6 mide, while absence of these responses
    in SJL mide may enable them to escape the disease. The preservation of
     the immunodominance of peptide 140-162 in the 1 cent residuant on a belief
     probably most important for the pathogenesis of WAMA in this evenue.
II 157960-63-9
    RL: BIOL (Biological study)
        (in B- and T-dell epitope mapping on adetylcholine receptor .alpha.
        chain, autoimmune myasthenia gravis in relation to;
L15 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                   1994:318925 HCAPIUS
DOCUMENT NUMBER:
                       111:31360
                       Diagnosis of tumors by assay of CD44 splicing patterns
                       Tarin, David; Matsumura, Yasuhiro
FATENT ASSIGNEE (S):
                     ISIS Innovation Ltd., UK
                       PCT Int. Appl., 41 pp.
SOURCE:
                       -corem: PIKKP2
                       Patent
LANGUAGE:
                       Enalish
PANILY MOO. NYM. 3 YMM: 1
PATENT INFORMATION:
    PATENT NO. BANK CALL
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BW: AI, BE, CE, IE, IF, ES, FR, CE, CR, IE, IT, IU, MO, MI, PT, SE
            EP 801822 A1 1998081 EP 1993-916109 19980720
            EP 651822 E1 19960417
                 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE
          TOP 08800731 T2 18460131 TP 1993-804278 19930720

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              EM: AT, BE, CH, DE, DE, ED, EF, PP, PP, IF, IT, IN, WY, IX, FI, CE
           CA 2149636 AA 18441614 CA 188-114968 188-11111
EP 672130 A1 18860917 EF 1884-807248 18831121
R: AT, BE, CH, CE, CK, ES, FR, SB, CF, IE, IT, HI, LT, MC, CL, FT, SE
           us 5530646 à la ligadina de la laceta de laceta de la laceta de la laceta de la laceta de la laceta de laceta de la laceta de lace
           US 8809898 A 19073819 US 1998-428188 17483810
RITY APPLN. INFO.: 3B 1992-18478 174820001
3B 1992-24387 17721120
PRIORITY APPLN. INFO.:
                                                                                              ## 1992-26165 19921216
WO 1993-GB1520 19930720
                                                                                              WD 1993-GB2394 19931122
         There is marked over-expression of multiple spliced variants of the CD44
AB
           gene in tumor compared to counterpart normal tissue. This observation
            forms the basis of a method of diagnosing neoplasia by anal. of a sample
           of body tissue or body fluid or waste product. A new exon 6, of 129 bp,
           has been found and sequenced, and is claimed as such and for use in the
           diagnostic method. Samples of breast tumors were assayed for CD44 mRNA by
           reverse transcription/PCR using primers to detect hemopoletic CD44
            followed by hybridization with a probe from exon 4. A no. of splice
           variants were found in neoplastic tissue that were absent from normal
           tissue, this was found in all patients tested. There was a difference in
           splice patterns between neoplastic and non-neoplastic diseased tissues
           (dystid disease). Similar results were found in dolon dander using biopsy
           and stool samples and in bladder cander using urine samples for diagnosis.
           155216-25-4
           RL: PRF 'Properties
                   (amino acid sequence of, in neoplastic tissue, altered splicing
                  patterns in neoplastic tissue in relation to)
L15 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:564026 HCAPLUS DOCUMENT NUMBER: 117:164026
                                                           Species- and subtype-specific recognition by antibody
TITLE:
                                                          WF6 of a sequence segment forming an
                                                           .alpha.-bungarotowin binding site on the hisotinic
                                                           acetylcheline receptor .alpha. subunit
AUTHOR(S):
                                                          Molane, K. E.; Fritzen, M.; Wu, N.; Diethelm, B.;
                                                          Maelicke, A.; Conti-Tronconi, B. M.
                                                          Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN,
CORPORATE SOURCE:
                                                          55108, USA
                                                           Journal of Receptor Research (1990), 10 3 , 1994-31
SOURCE:
                                                           ONDEN: TERROW; ICON: 187-11
DOCUMENT TYPE:
                                                           LAND AGE:
                                                           The monoclonal antibody WFC competes with aperplohetime and
AΒ
           .alpha.-bungarotoxin (.alpha.-BGT) for binding to the Torpedo nicotinic
           adetylcholine redeptor (nAChR) .alpha.l subunit. By using synthetic
           peptides corresponding to the complete Torpedo nAChR .alpha.1 subunit, the
           authors previously mapped a continuous epitope recommized by WF6, and the
           prototope for .alpha.-BST, to the sequence segment .alpha.1,181-0000.
           Single amino abid substitution analogs have been used as an initial
           approach to det. the mit. amino solds for WFE and . Apple.-POT binding.
           In the present study, the suthers rentinue the anal. of the structural
           features of the MF6 epiture by comparing its cross-reactivity with
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33 86-1565 116 KIN414

synthetic pertides of reen hains to the .askna. Documents in hotie harme and lalpha. Total The country ear, and the courte fraction, agree - below in a nagratein subunits, ... ipha.P-FTEF ... ipha.l and ... ipha.B-FTEF ... ipha.c. The results indicate that WFO is able to onoss-react with the muscle lalpha.1 subunits of different species by virtue of conservation of several crit. amine arid restitues between positions 197-198 of the .alpha.1 subunit. These studies further define the essential structural features of the sequence segment .alpha.1 (181-200) required to form the epitope for WF6.

133295-54-2 133322-53-9

FI: BITL Bi logical study

can thody to himber recept a bungarot win binding site kinding by, structure in relation to)

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ACCESSION NUMBER: 1991:223857 HCAPLUS

DOCUMENT NUMBER: 114:223857

TITLE: Structural determinants of .alpha.-bungarotomin

> binding to the sequence segment 181-200 of the mussle nizetiĥio amegžeĥsile av begt e la gela se esteit:

eifens of motele contact the contact is

species-specific amino acla substitutions

McLane, Kathryn E.; Wu, Miadong; Diethelm, Brenda; AUTHOR(S):

Conti-Tronconi, Bianca M.

Coll. Biol. Sci., Univ. Minnescta, St. Paul, MN, CORPORATE SOURCE:

55108, USA

Biochemistry (1991), 30(20), 4925-34 SOURCE:

GODEN: BIGHAW; ISSN: 0006-2960

Joarnal LANGUAGE: English

The sequence segment 181-200 of the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha. subunit forms a binding site for .alpha.-bungarotoxin (.alpha.-BTX). Synthesis peptides corresponding to the homologous sequences of human, calf, mouse, chicken, frog, and cobra muscle nAChR .alpha.1 subunits were tested for their ability to bind 125I-.alpha.-BTX, and differences in .alpha.-BTX affinity were detd. by using soln. (IC50) and a solid-phase (Kd) assays. Panels of overlapping peptides corresponding to the complete .alpha. I subunit of mouse and human were also tested for .alpha.-ETM binding, but other sequence so ments forming the .alpha.-BTK site were not consistently detectable. The Torpedo .alpha.1(181-200) and the homologous frog and chicken peptides bound .alpha.-BTX with higher affinity (Kd .apprx. 1-2 .mu.M), ICES .apprx. 1-2 .mu.Mo than the human and half peptides (Md .apprx. 3-5 .mu.M, ICEO .apprx. 15 .mu.M). The mouse peptide bound .alpha.-FTM weakly when attached to a solid support (Kd .apprk. 8 .mu.M) but was effective in dompeting for 1231-.alpha.-BTM in soln. IDFO .apprm. 1 .mu.M . The obbra nAChR .alpha.1-subunit peptide did not detectably kind .alpha.-BIM in either assay. Amino acid substitutions were correlated with .alpha.-BTX binding activity of peptides from different species. The role of a putative visinal disulfide bond between systeine-192 and -193, relative to the Torpedo sequence, was detd. by modifying the peptides with sulfhydryl reagents. Rein. and alkylation of the peptides decreased .alpha.-BTX binding, whereas oxidn. of the peptides had little effect. Modifications of the dysteine dystine residues of the dobra peptide failed to indude .alpha.-PTK binding activity. Thus, while the adjacent cysteines are likely to be involved in forming the tomin . Alpha. 1-subunit interface a vicinal disulfide bound was not required for .alpha.-BTM kindin:.

133295-54-2P 133322-53-9P

RI: SEN (Synthetic preparation); FREF Preparation) (preph. and .alpha.-bundardtoxin binding by, toxin binding site of nicotinio anatylaholine receptor . Alpha. A chunit in relation to

133295-53-1P

Bl: SEU Synthetic preparation : 18EE largeration

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116 AMSWER 14 OF 17 HOMPLUS COPYRIGHT 2003 ACS
                      1990:525235 HCAPLUS
DOCUMENT NUMBER:
                         113:124235
Interaction of a smake venom mount win and a sequence
                         from the a weight mulling receptor only nated as mit
ACTHOR 8:
                         Bothmer-By, Akrol A.; Mishri, F. K.; Low, Birkari W.
CORPORATE SUURCE:
                         Dep. Chem., Carnegie Mellon Univ., Fittskurdh, FA,
                         15013, TSA
                         UCLA Symposia on Molecular and Collular Filling, New
SOURCE:
                         Series 1997, 199 Front. MAR M. 1. 8191. , 1994.
Oli BM: MaMH: 8; 108M: 1099 - 849
                         James 1
                         English.
AB .alpha.-Cobratowin and acetylon line receptor .a.pha.-subunit
     complementary binding domain poptide Tresidues 179-191) were studied by
    1-D and 2-D IMR spectroscopy. A model for binding is proposed.
    114753-46-7
     RL: BICL (Biological study)
        (.alpha.-cobratexin binding by, conformation in, NMR study of)
L15 ANSWER 15 OF 17 HOAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                         1988:500189 HOAFLUS
DOCUMENT NUMBER:
                         109:106189
TITLE:
                         Binding of .alpha.-bungarotoxin to synthetic peptides
                         corresponding to residues 173-204 of the .alpha.
                         subunit of Torpedo, calf, and human acetylcholine
                         receptor and restoration of high-affinity binding by
                         sodium dodecyl sulfate
                         Wilson, Faul T.; Lentz, Thomas L.
AUTHOR(S):
CORPORATE SOURCE:
                         Sub. Med., Tale Thir., New Haven, Tr, T. 1 , Tok
SOURCE:
                         Bischemistry (1966), 27 18 , err - 4
                         CODEN: BICHAW; ISSN: 0018-2800
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         English
AB To investigate structure-function relations of a segment of the
     acetylcholine receptor .alpha. subunit, binding of .alpha.-bungarotoxin to
     synthetic peptides corresponding to residues 173-204 of Torpedo, calf, and
     human .alpha. subunits was compared using a solid-phase radioassay. The
     affinitles of 1881-labeled .alpha.-bungarotomin for the calf and human
     peptides were 15- and 150-fold less, resp., than for the Torpedo peptide.
     On the basis of nonconservative substitutions in the calf and human
     sequences, arom. residues (Tyr-181, Trp-187, and Tyr-189) are important
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for the higher affinity binding of the Torpedo peptide. Substitution of neg. charged Glu-180 with uncharged Gln in the calf peptide did not significantly affect toxin binding, indicating Glu-180 alone does not comprise the anionic subsite on the receptor to which the cationic quaternary ammonium groups of cholinergic agents bind. d-Tubecurarine competed with towin binding to the modified values: Former which large Glu-180 and Asp-180 present in Torpedo. Thus, the most subsite obult be formed by another neg. charged residue or by 31 amino abiliside shain. It is possible that the pos. charges on challinergic ligands are countered by a neg. electrostatio potential provided by polar groups, such as the hydroxyl group of typosine, present on several residues in this region, and the neg. charges present on any of residues 178, 187, 187, or 177. Equil. sath. binding of .alpha.-bunggrot win to Toppe to peptite 173-274 révealed a minor bindir romponeum with an aparent Wolt 1.0 mM and a major component with a KU of 65 mM. In the presence of 1.71 sps, 1 binding component with a RT of 1.9 nM was defected. This compares with an affinity of RD = 0.41 nM for towin binding to native acetylcholine receptor in the solid-phase assay. 3DS may stabilize a conformation of the pertide that is conductive to high-affinity binding.

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115826-29-4 115826-30-7
    RI: FIXL (Biolivii wi story
         Bungarotomin kinding to, nipotini o relegion konding in relation to
115 AMEWER 16 OF 17 HOAPLUS CHEYRIGHT 1. 8 ACS
                         1988:4 L.T1 HOAF100
DOCUMENT NUMBER:
                        .alpha.-Tomin binding to abetyl Holine reserve
                         laipha.179-191 peptides: intrinsic fluores ende
                        studies
LITHOR :
                        Radding, W.; Corfield, F. W. R.; Levinson, L. S.;
                        Hashim, G. A.; Low, B. W.
                        Howard Hughes Inst., Columbia Univ., New York, NY,
CORPORATE SUURCE:
                        10032, USA
                         FEBS Letters (1988), 231(1), 212-16
SOURCE:
                        CODEN: FEBLAL; ISSN: 0014-5793
                         Journal
iniguage:
                         English
AB Interactions between 2 .alpha.-toxins and the synthetic peptides
     .alpha.179-191 from both dalf and human abetylchiline receptor
     .alpha.-subunit sequences were studied by measurements of quenching of
     intrinsic fluorescence after toxin addn. Dissoon. consts. of .apprx.5
     .times. 10-8M for binding of calf peptide by both .alpha.-cobrotoxin and
     erabutowin a were estd. The binding of .alpha.-cobrotowin to calf
     peptide, which leads to marked quenching of fluorescence intensity, is
     inhibited by a 114M excess of acetylcholine. The human .alpha.179-191
     peptide binds to .alpha. + soprotemin, but not, under comparable sonditions,
     to erabutoxin a.
    114753-46-7P
    RL: SPN (Synthetic preparation); PREP (Preparation)
        (prepr. of, of salf asetylcholine receptor .alpha.-subunits, and
        .alpha.=toxins binding by)
L15 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2003 ACS
                    1984:185956 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                        100:195956
TITLE:
                        A super active cyclic hexamentide analog of
                        somatostatin
AUTHOR(S):
                        Veber, Daniel F.; Saperstein, Richard; Nutt, Ruth F.;
                        Freidinger, Roger M.; Brady, Stephen F.; Curley, Paul;
                         Perlow, Debra S.; Paleveda, William J.; Colton, C.
                         Dylion; et al.
CORPORATE SOURCE:
                        Merck Sharp and Dohme Res. Lak., West Foliat, IA,
                         19486, 1026
SOURCE:
                         life Shierness 1 -- 4 , -4 14 , 1 - 1 --
                         00DEN: LIFSAK; ISSN: 7024-32 78
DOCUMENT TYPE:
                        Journal
                        English
LANGUAGE:
AB Cyclo(N-methyl-Ala-Tyr-D-Trp-Lys-Val-Fhe) (I) [81377-02-8] was
     50-100-fold more potent than syclic schatostatin [38916-34-6] for the
     inhibition of insulin [9004-10-9], glucagon [9007-90-5] and growth
    hormone [9001-71-6] release as revealed by structure-activity studies of
     cyclic hemapophide analogs of sematestatin in rats. The hydromyl group of
    tyrosine conterred a 10-fold enhancement to the potency. Fotency was also
    correlated with hydrophobicity. I improved the control of postprandial
     hyperglycemia in diabetic animals when given in combination with insulin.
    The analog was guite stable in the blood and in the gastrointestinal
    tract, but the bicavailability after oral administration was only 1-3%.
     The biol. properties and long duration of I should allow blin. evaluation
    of the inhibition of glucamon release as an adjunct to insulin in the
    treatment of patients with Higheres.
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89808-58-2

RL: PICL Billsing study

somator ropin secretion inhibition by, structure in relation to,

E4 THROUGH E28 AGSIGNED => fill req FILE 'RESISTRY' ENTERED AT 13:88:20 ON 18 FEB 2003 USE IS SUPJECT TO THE TERMS OF YOUR STU SUSTOMER AGREEMENT. PLEASE SEE "HELF USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Themis will distribute And Property values tagged with Indianalists one of a Villing and pure provided by Intuchen. STRUCTURE FILE UPDATES: 12 FEB 2003 HIGHEST RN 489898-88-1 DISTIONARY FILE UPDATES: 12 FEB 2003 HIGHEST RM 489398-88-1 TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002 Tlease note that search-term pricing free apply when conducting SmartSELECT searches. Crossover limits have been increased. See HELP CROSSOVER for details. Experimental and calculated property data are now available. See HELP PROFERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details: http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf => => => s e4-e28 and 112 1 114753-46-7/PI (114753-46-7/RN)1 133299-54-2 HI 133095-54-0 FM 1 133322-83-9,81 (133322-53-9/RN) 1 115826-29-4/BI (115826-29-4/RN) 1 115826-30-7/BI /115826-30-7/RNY 133295-53-1/RI (133295-53-1/RN) 1 155217-25-4 91 (180216-28-4 RN 157960-63-9/BI (157960-63-9/RN) 1 170662-94-9/BI (170662-94-9/RN) 1 170662-99-3/BI IT 1662-98-3.BM $-1.776 \, (2 \, \mathrm{kg}) = (2 \, \mathrm{kg}) \, (2 \, \mathrm{kg})$ 17...

1= 113-11-1 500

10 10 - 10 - 50

1 1 6 6 3 - 10 - 1 BI

1 171663-14-3 81

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177443-73-3380
              171663-14-4,81
                  1771663- 4-4°EN
             1 17,397-35-1 31
             102990-30-27810
1 1 11127- --- 1 81
                 1 209192-30-00BI
                  (2081)2-3:-T.EM.
             1 209457-55-6/81
                  [209487-88-67FN]
             1 2:0:11:--- BI
                  (241814-51-7/RM)
             1 3:130.-38-1/81
                 1 4-270 -32-8/81
                 (432700-32-8/RN)
             1 434378-63-9/BI
                 (434378-63-9/RN)
             1 89808-58-2/81
                 789808-58-27RNY
116
            28 (114753-46-7/BI OR 183298-84-1/BI B 1 1932/4-18 BI B 1 1932/4-19
               -4/BI OR 115826-30-7/BI OR 138/95-83-1/BI SE 188/188/18-18-4 BI OF
               157960-63-9 BI OR 17 FEW-84-9 BI DE 10 FF - 9-9 BI DE 10 FE - 9-9
               4 PET CR 170483-0 -0080 08 17 683-010 BI 08 I 08 1 08 4 8-10 PE
               170663-03-3/BI OR 170663-04-4/BI OR 171997-35-2/BI OR 201529-09-
               1/BI OR 208192-30-7/BI OR 209457-55-6/BI OR 241814-51-7/BI OR
               301300-56-1/BI OR 432700-32-8/BI OR 434378-63-9/BI OR 89808-58-2
               /BI) AND 112
=> d .seq 116 1-25
116 ANSWER 1 OF 25 REGISTRY COPYRIGHT 2003 ACS
    434378-63-9 REGISTRY
RM
    L-Isoleudine, L-methionyl-L-seryl-L-tryptophyl-L-histidyl-L-seryl-L-
     tryptophyl-L-isoleucyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-.alpha.-glutamyl-
     L-isoleucyl-L-tyrosyl-L-leucyl-L-.alpha.-glutamyl-L-asparaginyl-L-threonyl-
     L-prolyl-L-cysteinyl-L-tyrosyl-L-lysyl-L-tyrosyl-L-.alpha.-glutamyl-L-
     threonyl-L-.alpha.-aspartyl-L-isoleucyl-L-leucyl-L-tyrosyl-L-isoleucyl-L-
     alanyl-1+seryl-L-phenylalanyl-L-.alpha.-aspartyl-L-phenylalanyl-L-seryl-L-
     arginyl-L-glutaminyl-L-isoleucyl-L-prolyl-L-seryl-L-threonyl-L-methionyl-L-
     arginyl-1-isoleupyl-1-seryl-1-valyl-1-tyrosyl-1-seryl-1-valyl- (901)
     INDEX NAME:
OTHER NAMES:
    3444: FN: WOO192503 SEQID: 844% blaimed protein
    Protein (human blone WO0191818-SEQID-8446 fragment
SQL 50
    434378-63-9 REGISTRY
RN
SQL 50
         1 MSWESWIFYS EIYDENTEDY KYETDILYIA DEDESEÇIFƏ TAKISVYƏVI
SEÇ
HITS AT: 3-8
REFERENCE 1: 137:10018
116 ANSWER 2 OF 05 REGISTRY COPYRIGHT 2003 ACS
B.1.
    432700-32-8 FERINTEY
    LeThreonine, LeginnaminyleLeasparaginyleLelencyleLethrecnyleLealanyleLe
    aluraminyl-L-.alpha.-aspartylplysyl-L-valyl-L-gluraminyl-L-tryptsphyl-L-
     cystoinyl-1-.alpha.-aspartyl-1-lau ylglycyl-1-soryl-1-lau yl-1-glutaminyl-
     LeprolyleLeprolyleLeleucyleLeprolyleLeseryleLeseryleLetryptophyleLe,alpha.e
     aspartyl-l-tyrosyl-l-arginyl-l-ardinyl-l-.alpha.-dluramyl-l-saryl-l-lenryl-
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Misselvey 13 312414

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I = wstainyl-i-prolyt-i-wayl-h-sayl-i-phanylalanyl-i-phanylalanyt-i-
    is led tylelephenylylany. - Letrypt. phylelelysylele arginylelet ypt. phylylydyle
    l-phenylalamyl- 201, OA INDER MAME,
CTHER NAMES:
- Protein (human clone W00164835-SEQID-26885 fragment)
SQL 47
    432700-32-8 REGISTRY
SQL 47
SEL 1 INTRIBUTE WINDERLIEF LESON FRED FLORESTE WERWER.
HITS AT: 41-46
REFERENCE 1: 150:1516
116 ANSWER 3 OF 25 REGISTRY CLEYRIGHT LIFE ANY
   301300-56-1 REGISTRY
CN L-Tyrosine, N-71-swohemadesyl7-L-threshyl-L-valyl-L-arginyl-L-scryl-L-
    -valyl-L-prolyl-L-trypt.phyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-
    phenylalanyl-L-histidylglycyl- (901) (CA INDEX NAME)
NTE modified
type ----- location ---- description
modification Thr-1
                               1-oxohexadecyl<Pal>
SQL 15
RN 301300-56-1 REGISTRY
SOL 15
SEQ 1 TVRSVPWTAW AFHGY
               HITS AT: 7-12
REFERENCE 1: 133:298 42
L16 ANSWER 4 OF 25 REGISTRY COPYRIGHT 2003 ACS
    241814-51-7 REGISTRY
RM
   L-Tyrosine, L-threonyl-L-valyl-L-seryl-L-arginyl-L-valyl-L-prolyl-L-
    tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-
    histidylglycyl- (901) (CA INDEX NAME)
OTHER NAMES:
CN 1: FN: W0020448T SEQID: E dlaimed protein
RN
   241814-51-7 REGISTRY
SQL 15
SEQ 1 TVSRVPWTAW AFHGY
               ----
HITS AT: ~-12
REFERENCE 1: 137:107904
REFERENCE 2: 136:117369
REFERENCE 3: 131:199416
116 ANOWER I OF OF BEGISTER OLITED BOTH AND
   209457-55-6 REGICTET
3.17
CN LeGerine, LelysyleLean sinyleLephonylal myleLelysyleLeal in minyleLe.alphaje
    aspartylalynylalynylaletayyt ahyleleskaylelebbstidyleletayat ahylelebasyle
    Lephenyl alanyleletayyt phylelesery. - + 71 - 7A 100 FW 17A49
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3.1 17
RN 209457-55-6 REGISTRY
SQL 17
JE, I BEFR, I SPACE HUNBAU.
HITS AU: 4-14
REFERENCE 1: 129:08489
L16 AMSWER 6 OF 25 REGISTRY COPYRIGHT 2013 Ans
   208192-30-7 FERISTRY
   - Slybine, L-alanyl-L-.alpha.-aspartylglybyl-L-alanyl-L-tryptophyl-L-
    pnenylalanyl-1-seryl-1-tryptophylglydyl-1-phenylalanyl-1-prolyl-1-
    glataminyl-L-tryptiphyl-L-tryptophylglybyl-L-alanyl-L-alanyl- (901) (CA
INDEX NAME)
3QL 18
   208192-30-7 REGISTRY
SQL 18
SEQ 1 ADGAMESWGE POWWGAAG
             HITS AT: 5-10
REFERENCE 1: 129:91863
L16 ANSWER 7 OF 25 REGISTRY COPYRIGHT 2003 ACC
RN
   201529-09-1 REGISTRY
CN L-Aspartic acid, L-tyrosyl-L-arginylglycyl-l-tryptcphyl-L-lysyl-L-histldyl-
    L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-thre nyl-L-byshainyl-L-
    cysteinyl-L-prolyl-L-.alpha.-aspartyl-L-threonyl-L-prolyl-L-tyrosyl-L-
    leucyl- (901) (CA INDEX NAME)
SQL 20
RN
   201529-09-1 REGISTRY
SQL 20
        1 YRGWKHWVFY TCCPDTFYLD
SEQ
            _ ::: = = = :::
HITS AT: 4-9
REFERENCE 1: 128:110913
L16 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN
   172997-35-2 REGISTRY
CN L-Lysinamide, L-threonyl-L-tryptophyl-L-, alpha. -aspartyl-L-tryptophyl-L-
    phenylalanyl-L-seryl-L-trypt:phyl-L-l-waryl-L-phonylalanyl-L-Loudyl-L-
    prolyl-1-seryl-i-.alpha.-slut appl-i-seryl- Fin i wa imba mun
NTE modified
              ----- location ----- description
terminal mod. Lys-15
                      - C-terminal amide
SQL 15
RN 172997-35-2 FEGISTRY
S.T. 15
SEÇ 1 TWOWESWLEI ESESK
            .. 1 11 12 17
HITS AT: 4-9
PHFFFFM: 1: 114:114:00-
```

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116 AMSWER 2 OF 15 REGINTRY COFFRIGHT 2 3 ACC
    170663-04-4 REGISTRY
    L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-
     aysteinyl-L-aystinyl-Likrolyl-L-threinyl-L-threonyl-L-histidyl-L-tyrosyl-
L-l-wayl- - this - sak inden name
     21
     170663-04-4 REGISTRY
341 21
         1 EARGWWHWUR YSOCRITHYL D
               ==:-:-=:-
HITS AT: 5-10
REFERENCE 1: 103:33:2013
116 ANSWER 10 OF 25 REGISTRY CONTRIBETOR SAME
EN 170663-03-3 REGISTRY
   L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylal myl-L-tyrosyl-L-seryl-L-
     cysteinyl-L-cysteinyl-L-seryl-L-threchyl-L-threchyl-L-prolyl-L-tyrosyl-L-
     leucyl- (9CI) (CA INDEX NAME)
SQL 21
    170663-03-3 REGISTRY
RN
SQL 21
SEQ
         1 EARGWKHWVF YSCCSTTPYL D
               HITS AT: 5-10
REFERENCE 1: 123:330219
116 ANSWER 11 OF 28 REGISTRY COPYRIGHT / 13 A'S
    170663-02-2 REGISTRY
RN
    L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-
     cysteinyl-L-tryptophyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-
     leucyl- (901) (CA INDEX NAME
SQL 21
    170663-02-2 REGISTRY
EN
SQL 21
SEQ 1 EARGWRHWVF YSCWFTTFYL D
HITS AT: 5-10
REFERENCE 1: 123:330219
116 ANSWER 12 OF 25 REGISTRY COPYRIGHT 2003 ACS
BN
    170663-01-1 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
    L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-
     cysteinyl-L-cysteinyl-L-prolyl-L-threchyl-L-threchyl-L-prolyl-L-tyrosyl-L-
    leubyl-1(901)1 (CA İMDEXÎMAMÊ
SQL 21
    170663-01-1 REGISTRY
RN
SQL 21
SHQ I EAR WEREVER TO TETTING I
HITS AT: 5-17
REFERENCE 1: 103:39:219
```

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Illo ANGWER 13 OF OF RESIDENCE OF FYFIGHT USES AND
    170663-00-0 REGISTRY
    - L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arqinylgly.yd-L-trypt.phyl-
     L-lysyl-L-histidyl-L-tryptcphyl-L-valyl-L-phenylalanyl-L-tyr syl-L-alanyl-
     Lemysteinylelemysteinylelepholylelethae nylelethae nylelepholyleletyrosyle
Lelephyle (401 – 7A INLEK DAME)
21
EN 170663-00-0 RESIDTEY
3 <u>%</u> 21
SEÇ 1 EARGWKHWUF YACOPTTPYL C
H1TS AT: 5-10
REFERENCE 1: 123:330219
116 AMSWER 14 OF 18 REGISTRY COPYRIGHT 2003 AGS
RN 170662-99-4 REGISTRY
   — L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-ryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-
     L-cysteinyl-L-cysteinyl-L-leucyl-L-threcnyl-L-threonyl-L-prolyl-L-tyrosyl-
     L-leucyl- (901) (CA INDEK NAME)
SQL 21
RN 170662-99-4 REGISTRY
SQL 21
         1 EARGWKHWMF YACCOTTERE D
SEQ
               ===:::==
HITS AT: 5-10
REFERENCE 1: 123:330219
L16 ANSWER 15 OF 25 REGISTRY COPYRIGHT 2003 ACS
F_nN
    170662-98-3 REGISTRY
   L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-
     L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-
     tyrosyl-L-leucyl- (901) (CA INDEX NAME)
SQL 21
     170662-98-3 REGISTRY
EN
SOL 21
SEQ 1 EARGWKHWVF YACCFTTHYL D
HITS AT: 5-10
REFERENCE 1: 128:330219
116 ANSWER 16 OF 28 REGISTRY COPYRIGHT 2003 ACS
    170662-94-9 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyr syl-L-alanyl-
     Le systeinglele systeingleheldsbylehethra anglehethra anglehethra idglehe
     tyrosyl-L-leusyl- (901) (CA INDEM MAME)
SQL 21
RM 170662-94-9 REGISTRY
S.L 21
         1 HAB WARNEY BACOLTINEL T
              :: := = .::
HITH AT: 7-17
```

```
REFERENCE 1: 1.3:331214
116 AMSWER 17 OF 18 PESICIFY COPYRIGHT LOSS AND
    157960-63-9 REBISTRY
    l-Tyrosine, L-arginylyly syl-l-tryptophyl-l-lysy"-l-histidy)-l-tryptophyl-L-
     79 7 <del>4</del>
6 20 42
    17
    157960-63-9 REBISTRY
SQL 17
SEQ
        1 RGWKHWUFYS COPTTRY
           5. . . . . . <del>.</del>
HITS AT: 3-8
REFERENCE 1: 121:203/99
116 ANSWER 18 OF 28 REGISTRY CUPYRIGHT 2018 ACC
EX
    155216-25-4 REGISTRY
    - L-Alamine, L-threchyl-L-legbyl-L-methichyl-L-seryl-L-threchyl-L-beryl-L-
     alanyl-L-threenyl-L-alanyl-L-threenyl-L-. alpha.-alutamyl-L-threenyl-L-
     alanyl-L-threonyl-L-lysyl-L-arginyl-L-glunaminyl-L-.alkha.-glutamyl-L-
     threonyl-L-tryptophyl-L-.alpha.-aspartyl-L-tryptophyl-L-phenylalanyl-L-
     seryl-1-tryptophyl-1-leucyl-1-phenylalanyl-1-leucyl-1-prolyl-1-seryl-1-
     .alpha.-glutamyl-L-seryl-L-lysyl-L-asparaginyl-L-histidyl-L-leucyl-L-
     histidyl-L-threonyl-L-threonyl-L-threonyl-L-glutaminyl-L-methionyl- (901)
     (CA INDEX NAME)
OTHER NAMES:
    Antigen CD 44 (human exon 6)
CN
SQL 43
RN
    155216-25-4 REGISTRY
SQL 43
SEC
        1 TLMSTSATAT ETATKROETW DWFSWLFLPS ESKNHLHTTT OMA
HITS AT: 22-27
**RELATED SEQUENCES AVAILABLE WITE SECLINE:
REFERENCE 1: 120:318418
L16 ANSWER 19 OF 25 REGISTRY COPYRIGHT 2003 ACS
    133322-53-9 REGISTRY
    L-Aspartic acid, L-alanyl-L-arginylglycyl-L-tryptcphyl-L-lysyl-L-histidyl-
CN
    L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinvl-L-
     cysteinyl-1-prolyl-1-threcnyl-1-threcnyl-L-prolyl-1-tyrosyl-1-leucyl-
    (901) (CA INDER NAME)
SQL 20
    133322-53-9 REGISTRY
7.7
SQL 20
        1 ARGWKHWUFY SCCETTEYLD
SEÇ
             === ···==······==
HITS AT: 4-9
REFERENCE 1: 117:1/401/
REFERENCE L: 114:70.5507
LIC ANSWER 21 OF LE REGISTRY LIPTRIGHT LOGGERY
    133295-54-2 PEGINTRY
CN L-Aspartin and, L-sexyl-L-arginylglynyl-l-tryntymyl-L-lysyl-L-histidyl-L-
    tryptophylalavalylalaphonylalanylalanylalatys sylalaalanylalaoystajnylala
```

图 89 15 9 17 812414

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systeinyl-l-pr lyl-l-seryl-l-thro nyl-l-pr.lyl-l-tyr.syl-l-lousyl- 901
     CA INDEX NAME
S_L 20
   133295-54-2 FEGISTRY
SQL 20
   HITE AT: 4-2
REFERENCE 1: 117:164026
REFERENCE 2: 114:223957
LIG ANSWER 21 OF 25 REGISTRY CURYRIGHT WILL ACS
RD 133295-53-1 REGISTRY
   - L-Serine, L-.alpha.-gluramyl-L-serylglybyl-L-.alpha.-glutamyl-L-tryptophyl-
     L-valyl-L-isoleucyl-L-lysyl-L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-
     tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-
     tyrosyl- (MCI) (CA INDER NAME
SOL 20
RN
    133295-53-1 REGISTRY
SQL 20
        1 ESSEWVIKEA ROWKHWUHYS
SEQ
                       =======
HITS AT: 13-18
REFERENCE 1: 114:223850
L16 ANSWER 22 OF 25 REGISTRY COPYRIGHT 2:13 ACS
    115826-30-7 REGISTRY
RN
    L-Histidine, L-serylglycyl-L-.alpha.-glutamyl-L-tryptcphyl-L-valyl-L-
    methicnyl-L-lysyl-L-.alpha.-glutamyl-L-senyl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-
     threonyl-L-dysteinyl+L-dysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-
     tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl-
    (901) (CA INDEX NAME)
SQL 32
    115826-30-7 REGISTRY
RN
SQL
    32
SEQ
        -1 SGEWYMKESR GWKHWVFYTC CPSTPYLDIT YH
HITS AT: 12-17
REFERENCE 1: 109:106159
116 ANSWER 23 OF 25 REGISTRY CUPYRIGHT I 13 Ans
    115826-29-4 REGISTRY
    L-Histidina, L-sarylaly wl-1-. alpha.-a. dary.-1-trypt phy.-1-ta.yl-1-
    isolewcyl-l-lysyl-l-:lutaminy.-l-seryl-l-:riny.gly-yl-l-trypt.ghyl-l-
    lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-
    oysteinyl-L-dysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-tyrosyl-L-
    leucyl-L-.alpha.-aspartyl-L-iscleucyl-L-threcnyl-L-tyrosyl- (901) (CA)
    INDEX MAME
SQL
    32
3.7
    115826-29-4 BENISTRY
    32
SEC
        1 SGEWVIKOSE GWKHWVFYRO OPSTEYLDIT YH
                     HITS AT: 12-17
```

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REFERENCE 1: 1 :: 1 :: 1 :: 1
116 ANSWER 24 OF 28 REGIOTRY CORPRESET LIDS ACS
   114753-46-7 REGISTRY
   - L-Alanine, L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-
    L-lysyl-L-mistidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl- (201)
S_L 13
   114753-46-7 REGISTRY
SQL 13
SEQ 1 KESRGWKHWU FYA
         :-- -: = :- =
HITS AT: 6-11
REFERENCE 1: 113:128235
REFERENCE 2: 109:2071
116 ANSWER 25 OF 25 REGISTRY CUPYRIGHT A Us ANS
F.N
   89808-58-2 REGISTRY
CM Cyclo(N-methyl-L-alanyl-2-icdo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-
   L-tryptophyl) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN 1,4,7,10,13,16-Hemaazadyclooctadecane, cyclic peptide deriv.
CN Cyclic(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-
   - valyl-l-tryptophyl)
NTE systes
    modified
type ----- location ----- description
modification Ala-1
                             - methyl<Me>
modification Phe-2
RN 89808-58-2 REGISTRY
SQL 6
SEQ 1 AFWKVW
          HITS AT:
          1-2, 3-6
```